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OM nucleic - nucleic search, using sw model
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Searched:
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Gapop 10.0 , Gapext 1.0
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Listing first 45 summaries
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Copyright (c) 1993 - 2000 Compugen Ltd.
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em_htg_hum7:*
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gb_ph:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| m | ~1 | • | (11 | c 4 | (4) | K) | L L | Result |
|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|--------------------|-------------|
| 332 | 332 | 791 | 802 | 802 | 1746.4 | 2804.2 | 2948.2 | Score |
| 11.3 | 11.3 | 26.8 | 27.2 | 27.2 | 59.2 | 95.1 | 100.0 | Query |
| 340000 | 165942 | 170677 | 182344 | 155913 | 2250 | 2805 | 2949 | Length DB |
| 9 | 92 | 78 | 81 | 81 | 94 | 91 | 89 | DB |
| APOUL699 | AP001605 | AL138932 | AL445230 | AL513282 | AF240469 | D87442 | AF240468 | ID |
| APOOLO33 nomo sapi | APUULBUS HOMO Sapi | ALLISUSZ HOMO Sapi | AL445230 Homo sapi | AL513282 Homo sapi | AFZ40469 Mus muscu | D8/442 Human mkNA | AF240468 Homo sapi | Description |

em_or:*

| | CENE | REFERENCE AUTHORS TITLE | SOURCE ORGANISM | RESULT 1 AF240468 LOCUS DEFINITION ACCESSION VERSION | | | | 30 30 30 32 34 33 | 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 | 116 117 118 119 | 11 12 13 | c 10 |
|--|--|--|---|--|------------|---|--|---|--|--|---|--------------------------|
| ., Kawarai, T., Supala, A., Kawarai, T., Supala, A., raser, P.E. and St George)) Dept. of Medicine, Ce aases, University of Tor 18, Tanz Neuroscience Bl), Ontario M5S 3H2, Cana | Hassing the control of the control o | S., Levitan,D., Kawarai,T., Kawarai,T., Lie Milman,P., Lie Smith,M., Janufbi,S., Bruni,cbi,S., Bruni | ens Metazoa, Chordata, Craniata, Eutheria, Primates, Catarrhini | AF240468 2949 bp mRNA PRI Homo sapiens nicastrin mRNA, complete cds. AF240468 AF240468.1 GI:9992877 | ALIGNMENTS | 1.6 267759 1.6 14955 1.6 152513 1.6 165608 | 1.6 58998 63 1.6 215711 4 1.6 228479 5 1.6 139524 78 1.6 5809 85 1.6 92775 90 | 1.7 148600 70 1.7 53522 9 7 1.7 53576 9 7 1.7 53577 9 1 1.7 190492 75 1.7 298166 77 1.7 1063 53 | | 6.1 108537 82 6.1 173152 70 8 6.1 246646 81 8 6.1 302665 81 6 4.9 4692 97 2.7 7218 10 | 8.7 190442 66 ACO 7.2 170677 78 AL1 6.1 148540 81 AL3 6.1 167253 90 AL4 | 6 11.0 150597 77 AC09005 |
| y. Zhang, L., Tandon, A., A., Aebersold, R., ge-Hyslop, P. H. Centre for Research in oronto and University Bldg., 6 Queen's Park nada | grp-1 signal | hang,I pala,A Y., Zh Y. Zha Frase | Vertebrata; Euteleostomi; Hominidae; Homo. | 08-SEP-2000 | | ACU8198 Homo sapi ACU79418 Mus muscu AF000580 Dictyoste AP003207 Oryza sat ACO87842 Rattus no | AC014104 Drosophil AC008205 Drosophil AE003749 Drosophil AE003749 Drosophil AC090444 Rattus no AB007974 Homo sapi AL441964 Human DNA | Homo mo sa Sequer Sequer Homo Homo | AL416479 T7 end of AF240470 Drosophil AC073970 Homo sapi AC073620 Homo sapi AC090206 Homo sapi AC079429 Mus muscu AC027353 Homo sapi | AL590397 Homo sapi AC026466 Homo sapi AL391275 Homo sapi AL391377 Homo sapi UZ4105 Homo sapien 166494 Sequence 14 | Mus n Homo Homo Homo Human | Homo |
| 2y Db Db Db | Db Db | y Qy . | Db Qy | ОУ ДЪ ОУ | Qy Db | Quer Best Matc | BASE (| | | | | FEATU |

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tches 2949; Conserv
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CDS
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                                                                                                                                                                                     361 CCACGTAGTAGAGAAAGAGGAGGACCTACAGTGGGTATTGACTGATGGCCCCAACCCCCC
                                                                                                                                                                                                             361 ccacgtagtagagaagaggaggacctacagtgggtattgactgatggccccaacccccc
                                                                                                                                                                                                                                                                                           301
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                                                                                          GCTCAACGCCACTCATCAGATTGGCTGCCAGTCTTCAATTAGTGGAGACACAGGGGTTAT
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/KETAINS LATION - MARAGGSGADPGSRGLLRLLSFCVILAGLCRGNSVERKIYIPL
KETAINS LATION - MARAGGSGADPGSRGLLRLLSFCVILAGLCRGPYNDYMULLESKH
FTRDLMEKLKGRTSRIJGCQSSIESDTGVIHVEKEEDLOWLFDGPRVPYMYLLESKH
FTRDLMEKLKGRTSRIJGCQSSIESDTRYVIKGCYQDHNLSQNGSAPFPFLCANQLE
ELQWNSLGNILAYEDFSFPIFLLEDENETKVIKQCYQDHNLSQNGSAPFPFLCANQLE
FINHAVISTATCMRRSSIQSTFSINPEIVCDPLSDYNVWSMLKEPINTTGTLKEDDRVV
VAATRLDSRSFEWNVAPGAESAVASFVTQLAAAAEALQKAFDVTTLPRNVMFVFFQGET
FDYIGSSRNVYDMEKGKFPQLENVDSFVELGQVALRTSLELMHTDDFVGKNESVRN
QVEDLLAYILEKSGAGVPAVILARENQSQPLPPSSLQRFLARNISGVVLABGGSTHN
KYVQSILDTABKINVSYPEMISPEDLNFVTDTAKALADVATVLGRALYLALAGGTNFS
DTVQADPQTVTRLLYGFIIKANNSWFQSILRODLRSYLGDGFLQHYIAVSSPTWTTW
QYALANLTGTVVNLTREQCQDPSKVPSENKDLYEXSWFQGFLRSNETDRLBRCVRST
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a 803 c 692 g 770 t 2 others
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signal transduction"
/note="type 1 transmembrane protein; similar to Mus musculus and Drosophila melanogaster nicastrin encoded by GenBank Accession Numbers AF240469 and AF240470; interacts //interacting proteins PS1, PS2, S182, and E5-1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="nicastrin"
/protein_id="AAG11412.1"
/db_xref="GI:9992878"
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/db_xref="taxon:9606"
/chromosome="1"
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100.0%; Pred. No. 0;
vative 0; Mismatches
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| 04 04 04 | 0 Db | Qy Db | 뭥 | | Qy | Db 49 | 2 | P 68 | ф | Qy | Db Qy | Db | Qy | DЬ | ρy | Db | Qy | D Qy | Db | Qy | Db | Qy | Db | Qy | Db | Qy | 윱 | Qγ | B 2 | Ş |
|----------------|--------|---|--|--|---|---|-----|--|--|---|--|---|--|---|---|------|--|--|---|--|---|--|--|--|---|--|-------|--|--|---------------------------------------|
| | | 1501 | 1441 | سن | 00 | 1321 | , i | 1261 | 1201 | 1201 | 1141 1141 | 1081 | 1081 | 021 | 1021 | • | 61 | 901 | 1 | 1 | 81 | 81 | 721 G | 1 | 661 T | 661 | 601 G | 01 | 541 0 | _ |
| | | caqaqtatttacqacactqctqaqaacattaatqtqaqctatcccqaatggctgagccc | TCGAAACATCTCTGGCGTTGTTCTGGCTGACCACTCTGGTGCCTTCCATAACAAATATTA | AGGAGGCCAAATCAGTCCCAGGCTCTCCCACCATCTTCCCTGCAGCGATTTCTTCTAGAG | caggaggccaaatcagtcccagcctctcccaccattttcccttgcagcgatttcttcgagc | gg.ugyagga.c.c.c.gy.c.aca.r.cygagaagg.y.gy.gy.c.gy.gy.c.g.c.g.c.g.c.g.c.g.c | | attagagctttggatgcacacagatcctgtttctcagaaaaatgagtctgtacggaacca | CGTGCAGTTAGAGAATGTTGACTCATTTGTGGAGCTGGGACAGGTGGCCTTAAGAACTTC | gtgcagttagagaatgttgactcatttgtggagctgggacaggtggccttaagaacttc | aacttttgactacattggcagctcgaggatggtctacgatatggagaagggcaagtttcc 1 | AAGGCACCTGATGTGACCACCCTGCCCCGCAATGTCATGTTTTTTTT | aaaggcacctgatgtgaccaccctgccccgcaatgtcatgtttgtcttctttcaagggga 1 | AGGGCTGAAAGCGCAGTGGCTTCCTTTGTCACCCAGCTGGCTG | ggggctgaaagcgcagtggcttcctttgtcacccagctggctg | | agggttgtggttgctgccacccggctggatagtcgttcctttttctggaatgtggccc | ttacaatgtgtggagcatgctaaagcctataaatacaactgggacattaaagcctgacga 9 | CAGCATCAACCCAGAAATCGTCTGTGACCCCCTGTCTGA | agctccatccaaagcaccttcagcatcaacccagaaatcgtctgtgac | TGCCATGCAGCTCTTTTCACACATGCATGCTGTCATCAGCACTGCCACCTGCCATGCGGCG | gccatgcagctcttttcacacatgcatgctgtcatcagcactgccacctgcatgcggc | GAGTGCTATCAAGATCACAACCTGAGTCAGAATGGCTCAGCACCAACCTTCCCCACTATG | cagtgctatcaagatcacaacctgagtkagaatggctcagcaccaaccttcccactat | GAAGACTITAGTTTCCCCCATCTTCTTCTTGAAGATGAAAATGAAACCAAAGTCATCAA 7 | gaagactttagtttccccatctttcttcttgaagatgaaaatgaaaccaaagtcatca | | ccagagtttgctcactgcagagaaatacagtggaattcgctgggcaatggtttggctt | TICTCTCCTAGTGTACAGTGCCCAAATGATGGGTTTTGGTGTTTACTCCAATTCCTATGG | # # # # # # # # # # # # # # # # # # # |
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (27-AUG-1996) to the DDBJ/EMBL/GenBank databases. Nobu-
Nomura, Kazusa DNA Research Institute, Gene Structure 1; 1532-3
Yana, Kisarazu, Chiba 292, Japan (E-mail:cdnainfo@kazusa.or.jp,
URL:http://www.kazusa.or.jp, Tel:0438-52-3930, Fax:0438-52-3931)
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KIAA0253.
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Human mRNA for KIAA0253
D87442
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                                                                                                                                                                                                                                      /cell_type="myeloblast"
/clone="HA7036"
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                                                                                                                                                                                                  /sex="male"
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Eutheria; Primates; Catarrhini; Hominidae;
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IQWNSLGNGLAYEDFSFPIFLLEDENETKVIKQCYQDHNLSQNGSAPTFPLCAMQLES
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CATCAACCCAGAAATCGTCTGTGACCCCCTGTCTGATTACAATGTGTGGAGCATGCTAAA
                                                                                                    GCATGCTGTCATCAGCACTGCCACCTGCATGCGGCGCAGCTCCAAAGCACCTTCAG
                                                                                                                         GAGTCAGAATGGCTCAGCACCAACCTTCCCACTATGTGCCATGCAGCTCTTTTCACACAT
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2; Mismatches
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REFERENCE

house mouse.

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom1;
Eukaryota; Metazoa; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 2250)

| 2065 tectcatetigatactetacityagactigagacgitggaaaagitat cogtgocoggatatt 232 | SOURCE ORGE | CESS | AF2404 LOCUS DEFINI | RESULT | Db 2 | Оу 2 | Db 2 | Оу 2 | Db 2 | Qy 2 | Db 2 | 2 | N | Qy 2 | N | | N | N | N | | - | | | 2 | - | 2 | $\stackrel{\sim}{\sim}$ |) k | 21 | 9 | Qy 21 | Db 19 | Оу 20 |
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| | use mouse. s musculus karyota; Metazoa; Chordata; Craniata; Vertebrata; Eutele | 240469 240469.1 GI:999287 | 240469 2250 bp mRNA ROD 08-SEP-2 s musculus nicastrin mRNA, complete cds. | | GTAAATATATATAATGAGTTTCATTAAAATAGATTATCCCAC 28 | gtaaatatatataatgagtttcattaaaatagattatcccac 294 | GTACTTTTTATTAAGCTGTAATATCTATTTTTGTTTTTGTCTTTTTCCT | | GCACATTAGGGTGGGCGTGCTGCGGGTGGGTATCCCACCTCCAGCCCACAGTGCTCAG | gcacattagggtggcgtgctgcgggtgggtatcccacctccagcccacagtgctcac | GCATCTCTGGGCTGAGCCTACTGTCTCCTTTCCCACTGTCCTTTCTCCAGGCCCTCAC | gcatctctgggctgagcctactgtctccttcccactgtcctttctccaggccctcagat | GGAAGGACATAAAAGGTTTAATGTCAGGGTCAAACTACATTGAGCCCCTGAGGACAGG | ggaaggacataaaaggtttaatgtcagggtcaaactacattgagcccctgaggacagg | | gecetgtacetetetetgeteeteacececacecetgtacecagecacettectgac | | tttaactccctagttacccaccctaatttgcccttcaggacccttctactttttcctt | | tcctcttccttctctactcatgccagattttgggattacaaatagaagcttcttgctcc | | gagaaataaattaaattgcctcccttcctccgctcccctttccccatcaccccttccccat | | tgggcctgtctcagattgggattaacataaaagagtggaactatccaaaagagacag | | tcacttcctagagcatctgtcccactgggacacaaccactaatttgtcactggaacct | GGGAGCCAGGAGCTGTGTCATACTGAGGAGGACCCCAGCTTTCTTGCCAGCTCAGCA | ICTCCCTCATCATCATCATCATACCAAAAACCAAAAACCAAAAAA | totcoctcatcgtcacotactgcatcaatggccaaaggcgatgtcactcctccactgcarg | TCATCGCCAGCAAAGAGCTTGAGTTGATCACCCTGACAGTGGGCTTCGGCATCCTCAL | | CTACTGAATACTCTACATGGACTGAGAGCCGCTGGAAAGATATCCGTGCCCGGATAT, 1 | ctactgaatactctacatggactgagagccgctggaaagatatccgtgcccggatatt 2 |

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Submitted (02-MAR-2000) Dept. of Medicine, Centre for Research in Neurodegenerative Diseases, University of Toronto and University Health Network, Rm. 118, Tanz Neuroscience Bldg., 6 Queen's Park Crescent West, Toronto, Onlario M5S 3H2, Canada Location/Qualifiers
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AL513282/c
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                                                                                                                                                                                                                                                                              taatttgtcactggaacctccctgggcctg 2375
                                                                                                                                                                                                                                                                                                                                                                      TCTCCCTGCCTGCTCTGAACTTTACTTCCCAGACCAGGTGTCCGGCTGGGAACAAACCAC 2217
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACGTCCTTTTYGTTGCTCCCCGAGAGCCAGGAGCTGTGTCTTACTGAAGAGGACTCTAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGGGCTTCAGCATCCTTATCTTCTCTCTCATCGTCACCTACTGCATCAATGCCAAAGCCG
                                                                                            PROGRESS
AL513282
Homo sapiens
                                                                                                                                          Homo
                                                                                                                                                                AL513282
                                                                      AL513282.5 GI:13162044
                                                                                                                  RESS ***, 8 unordered pieces.
                                                HTGS_PHASE1; HTGS_DRAFT
                                                                                                                                                                155913 bp
                                                                                                                                                                   DNA
                                                                                                                                             1 clone RP11-179G5, *** SEQUENCING
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              misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 153015 bases at least Q40
Consensus quality: 153938 bases at least Q20
Consensus quality: 154565 bases at least Q20
Insert size: 154213; sum-of-contigs
Insert size: 164818; 1.0% error; agarose-fp
Opality coverage: 6.89x in Q20 bases; sum-of-contigs Quality
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                On Feb 28, 2001 this sequence version replaced gi:13161719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      * NOTE: This is a 'working draft' sequence. It currently consists of 8 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           requests: clonerequest@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (25-FEB-2001) Sanger Centre,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center project name: bA179G5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           web site: http://www.sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center code:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center: Sanger Centre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     coverage: 7.27x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (bases 1 to 155913)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20838 20938; contig of 20838 bp in length
20839 20938; gap of
20939 50589; contig of 29651 bp in length
50590 50689; gap of
50690 81538; contig of 30849 bp in length
81539 81638; gap of
81638; gap of
81638; gap of
100 bp
81638 89782; contig of 8044 bp in length
89683 89782; gap of
100 bp
108106 108205; gap of
100 bp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             149396 149495; gap of 1800 bp in length 149496 153075; contig of 3580 bp in length 153076 153175; gap of 100 bp 153176 155913; contig of 2738 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    UK. E-mail enquiries: humquery@sanger.ac.uk Clone
                                                                                                                                                                                                                                            vector_side:left"
                                       /note="assembly_fragment:03283
fragment_chain:2"
                                                                                                        fragment_
                                                                                                                                                                                                                             20939.
                                                                                                                                                                                                                                                                       clone_end:T7
                                                                                                                                                                                                                                                                                                                                                               /clone_lib="RPCI-11.1"
                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:9606"
/chromosome="1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                /note="assembly_fragment:00478
fragment_chain:2"
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                                                                                                                                                                                                     /note="assembly_fragment:01236
                                                                                                                                                                                                                                                                                                    fragment_chain:1
                                                                                                                                                                                                                                                                                                                        /note="assembly_fragment:02743
                                                                                                                                                                                                                                                                                                                                                                                         /clone="RP11-179G5"
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                                                         94886
                                                                                                                                                                                                                                                         95066 TTAATGTCAGGGTCAAACTACATTGAGCCCCTGAGGACAGGGGCCATCTCTGGGCTGAGCC 95007
                                                                                                                                                                                                95006
                                                                                                                                                                                                                                                                                                                                         95126
                                                                                                                                                                                                                                                                                                                                                                                                  95246 CATGCCAGATTTTGGGATTACAAATAGAAGCTTCTTGCTCCTGTTTAACTCCCTAGTTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95306 CTCCCTTCCTCCCCTTTCCCATCACCCCTTCCCCATTTCCTCTTCCTCTCTCTCACT 95247
                2924 agtttcattaaaatagattatcccac 2949
                                                                                                                                   2804 gctgcgggtgggtatcccacctccagccccacagtgctcagttgttactttttattaagctg 2863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95426
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                                                                                                                                                                                                       2744 tactgtctccttcccactgtcctttctccaggccctcagatggcacattagggtgggggt 2803
                                                                                                                                                                                                                                                                                                                                                                                                                      2624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2504 catgccagattttgggattacaaatagaagcttcttgctcctgttttaactccctagttac 2563
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2144 cttgagttgatcaccctgacagtgggcttcggcatcctcatcttctccctcatcgtcacc 2203
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                                                                             GCTGCGGGTGGGTATCCCACCTCCAGCCCACAGTGCTCAGTTGTACTTTTTATTAAGCTG
                                                                                                                                                                                       TACTGTCTCCCACTGTCCTTTCTCCAGGCCCTCAGATGGCACATTAGGGTGGGCGT
                                                ttaatgtcagggtcaaactacattgagcccctgaggacaggggcatctctgggctgagcc
                                                                                                                                                                                                                                                                                                                              TGCTCCTCACCCCACCCCTGTACCCCAGCCACCTTCCTGACTGGGAAGGACATAAAAGGT
                                                                                                                                                                                                                                                                                                                                                tgctcctcacccccaccctgtacccagccaccttcctgactgggaaggacataaaaggt 2683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ctcccttcctccgctcccctttccccatcaccccttccccatttcctcttccttctctact 2503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCATACTGAGGAGGACCCCAGCTTTTCTTGCCAGCTCAGCAGTTCACTTCCTAGAGCATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tcatactgagsaggaccscagcttttcttgccagctcagcagttcacttcctagagcatc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TACTGCATCAATGCCAAAGCTGATGTCCTTTTCATTGCTCCCCGGGAGCCAGGAGCTGTG
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fragment_chain:4"
153176. 155913
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fragment_chain:4"
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/note="assembly_fragment:02750
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149496. .153075
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Pred. No. 2.6e-204;
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Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 176921 bases at least Q40
Consensus quality: 179919 bases at least Q30
Consensus quality: 179919 bases at least Q20
Insert size: 181144; sum-of-contigs
Insert size: 181578; agarose fp
Quality coverage: 5.35x in Q20 bases; sum-of-contigs Quality
Coverage: 5.28x in Q20 bases; agarose-fp
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On Mar 12, 2001 this sequence version replaced gi:13274828.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center project name: bA517F10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center: Sanger Centre
Center code: SC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AL445230 182344 bp DNA HTG 10-MAR-200 HOMO Sapiens chromosome 1 clone Rp11-517F10, *** SEQUENCING PROGRESS ***, 13 unordered pieces.
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                                                                                                                                                                                                                                                                                                                   6698 6797; gap of 100 bp in length 6698 42129; contig of 6697 bp in length 6798 42139; contig of 35332 bp in length 42130 4229; gap of 100 bp in length 54865 54964; gap of 100 bp 54965 62235; contig of 7271 bp in length 6236 62335; gap of 100 bp in length 6236 62335; gap of 100 bp in length 81627 81726; gap of 100 bp in length 81627 81726; gap of 100 bp in length 88612 89711; gap of 100 bp 88712 95096; contig of 6885 bp in length 95097 9751; contig of 6885 bp in length 95097 9751; contig of 5255 bp in length 97752 97851; gap of 100 bp 97752 97851; gap of 100 bp 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NOTE: This is a 'working draft' sequence. It currently consists of 13 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                as soon as it is available and the accession number will
107299 107398: gap of 100 bp 107399 136764: contig of 29366 bp in length 136765 136864: gap of 100 bp 136765 140326: contig of 3462 bp in length 140327 140427: gap of 101 bp 140428 164080: contig of 23653 bp in length 164081 164180: gap of 100 bp
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Best Local Similarity
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TCATACTGAGGAGGACCCCAGCTTTCTTGCCAGCTCAGCAGTTCACTTCCTAGAGCATC 19471
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pred. No. 2.6e-204;
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2564 ccaccotaatttgcccttcaggacccttctactttttccttcctgccctgtacctctctc 2623
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                                                                                                                                                                                                                                       Submitted (13-JUN-2000) Sanger Centre, Hinxton, Cambridgehhire, CB10 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clope requests: clonerequest@sanger.ac.uk on Jul 16, 2000 this sequence version replaced gi:8573815...
Assembly program: XGAP4; version 4.5 sequencing vector: plasmid; L08752; 100% of reads Chemistry: Dye-terminator Big Dye; 39% of reads Chemistry: Dye-terminator ET-amersham; 60% of reads quality: 156012 bases at least 040 consensus quality: 160965 bases at least 020 consensus quality: 164137 bases at least 020
                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                         HTG; HTGS_PHASE1; HTGS_DRAFT.
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                                                                                                                           Center project name: dJ244G5
                                                                                                                                                            Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
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                                                                                                                    --- Summary Statistics
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Insert size: 167677; sum-of-contigs
Insert size: 131821; 35.2% error; agarose-fp
Quality coverage: 3.70x in Q20 bases; sum-of-contigs Quality
coverage: 4.70x in Q20 bases; agarose-fp
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77556; contig of 7109 bp in length
77557 7056; gap of 100 bp
81110; contig of 3454 bp in length
81211 82231; contig of 100 bp
81232 82331; gap of 100 bp
81232 82331; gap of 100 bp
9168; contig of 9337 bp in length
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70448 77556; contig of 8292 bp
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                          163850 163849: contig of 3665
                                                                                                                           154871; qa
154872 154971; qa
                                       160085 160184: gap of 160185 163849: cont
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141880 143172; contid of 1293 br
143173 143372; gap of 100 bp
143273 150964; contid of 7692 br
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112373 120545: contig of 8173 bp
120546: gap of 100 bp
120646 140354: contig of 19709 b
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4822 4921: gap of 100 bp
4922 11645: contig of 6724 bp in length
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152656; gap of 1492 bp
153707; con+-
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160084: contig of 3604 bp
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29256: contig of 8768 bp in length
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57: contig of 15375 bp in length
gap of 100 bp
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32: contig of 3512 bp in length
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contig of 3413 bp in length
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                            2503 tcatgccagattttgggattacaaatagaagcttcttgctcctgtttáactccctagtta 2562
                                                                   Local
                                                                                                                                                                                                                                                                   TCATACTGAGGAGGACCCCAGCTTTTCTTGCCAGCTCAGCAGTTCACTTTCCTAGAGCAT 9232
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                                                                                                                                                                                        TCATGCCAGATTTTGGGATTACAAATAGAAGCTTCTTGCTCCTGTTTAACTCCCTAGTTA 9472
tgctgcgggtgggtatcccacctccagcccacagtgctcagttgtactttttattaagct 2862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="assembly_fragment:01448" 154972. .156380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="assembly_fragment:00033"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="assembly_fragment:00171"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="assembly_fragment:01559"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="assembly_fragment:00257"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="assembly_fragment:01585
fragment_chain:6
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fragment_chain:6"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    te="assembly_fragment:01027"
808. .154871
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 791; DB 78;
Pred. No. 2.4e-201;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 78; Length 170677;
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DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Db 106343 TGAGTTTGGCACTCTGATGGTGGGCTTTGGCATCCTCATCTTTCTCGTTGTC-ACTTATA 106401
Db 106461 TTACTAAAGAGGACCCTAGCTTTCTCTGCTGGCTCAGCAGTTCACTTCCTAGATTATTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Db 106402 CTCCATCAATGACAAAACTAATGTGGTTTTTTGTTGCT-CCCTTGAGCCAGGAGCTGTGTC 106460
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 613;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2923 gagtttcattaaaatagattatcccac 2949
                                                                                                                                                                                     106521 TCCCACAGGGACÁTAACCACTAGTTTGTCACCAGAACGTCTCTGGACCTGTCTCAGACTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2146 tgagttgatcaccctgacagtgggcttcggcatcctcatcttctccctcatcgtcaccta 2205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2206 ctgcatcaatgccaaagctgatgtccttttcattgctccccggggagccaggagctgtgtc 2265
                                                                                                                                                                                                                                        2266 atactgagsaggaccscagcttttcttgccagctcagcagttcacttcctagagcatctg 2325
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Homo sapiens genomic DNA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AP001605.1 GI:7670559
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/chromosome="21"
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Db 107092 ----TTTCTTTTTTTTTTTTAAATATATAAATATTGAGTTTCATTAAAATAGATAACCCC 107145
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                                          Asakawa, S. Shintani, A. Sasaki, T. Nagamine, K. Mitsuyama, S. Shintaraks, S. Shi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and sequencing consortium
Nature 405 (6784), 311-319 (2000)
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Homo sapiens genomic DNA,
AP001699 AL163244 BA000005
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|A<sub>1_</sub>hhromosome 21q, section 43/105.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                * e.mail: info-chr21@molgen.mpg.de

* URL: http://chr21.rz-barlin.mpg.c

AL163244: Submitted (10-Apr-2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                * Max-Planck Institute for Molecular Genetics,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         * URL: http://genome.gbf.de/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              160-8582, Japan,
* e.mail: nshimizu@dmb-med.keio.ac.jp
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Submitted (10-APR-2000) to the DDBJ/EMBL/GenBank databases. The Chromosome 21 Mapping and Sequencing Consortium: * RIKEN Genomic Sciences Center, Human Genome Research Group * Institute of Molecular Biotechnology, Genome Analysis * Keio University School of Medicine, Dept. of Molecular Biology * GBF, Dept. of Genome Analysis * Max-Planck Institute for Molecular Genetics (addresses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             info.genome@gbf.de
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    * URL: http://www.dmb.med.keio.ac.jp/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          * Institute of Molecular Biotechnology, Genome Analysis, Beutenbergstrasse 11, D-07745 Jena, Germany,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     * Mascheroder
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          * URL: http://hgp.gsc.riken.go.jp/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       * RIKEN Genomic Sciences Center, Human Genome Research Group, Sagamihara 228-8555, Japan, e.mail: hattori@gsc.riken.go.jp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   On May 30,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ihnestrasse 73, D-14195 Berlin,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GBF, Dept. of Genome Analysis,
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URL: http://genome.imb-jena.de/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Weg 1, D-38124 Braunschweig, Germany, * e.mail:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Germany,
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REFERENCE

MEDLINE JOURNAL TITLE

AUTHORS

(bases 1 to 340000)

REFERENCE

AUTHORS

SOURCE KEYWORDS VERSION

AP001699.1 Homo sapiens DNA.

GI:7768674

ORGANISM

sapiens

DEFINITION

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                                                                                                                 Db 204857
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 11.3%; Score 332; DB 91; Best Local Similarity 73.2%; Pred. No. 8.3e-78; Matches 613; Conservative 2; Mismatches 152;
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Wall, R., Wang, S., Ward-Moore, S., Warren, R., Washington, C.,
Wall, R., Wang, S., Ward, M., V., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D.
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                                                                                         Submitted (14-FEB-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Mar 4, 2001 this sequence version replaced gi:13162443.
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is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
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NOTE: This is a 'working draft' sequence. It currently consists of 60 contigs. The true order of the pieces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           as soon as it is available and the accession number will be preserved.
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Consensus quality: 12348 bases at least 040
Consensus quality: 136820 bases at least 030
Consensus quality: 142590 bases at least 020
Estimated insert size: 124022; sum-of-contigs estimation
Quality coverage: 0x in 020 bases; agarose-fp estimation
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Contact: hgsc-help@bcm.tmc.edu
Project Information
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                                                                                                                                                                                   SEQUENCE, 6 unordered pieces AC074310
                                                                                                                                                                                                                AC074310 223431 bp DNA HTG 31-MAR-2.
Mus musculus chromosome 1 clone RP23-137120, WORKING DRAFT
                                          1 (bases 1 to 223431)
Rahhal,R., Yao,Z., Gu,W. and Roe,B.A.
Mus musculus Chromosome 1 BAC Clone rp23-137120
 Rahhal, R., Yao, Z.,
                             Unpublished
                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Muripae; Mus
                                                                                                                          Mus musculus
                                                                                                                                                     HTG; HTGS_PHASE1; HTGS_DRAFT
                                                                                                                                                                      AC074310.18 GI:13491228
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Db 146686 CCGACACCCCCCCATATTCAGCCACCTGCTGCACCAGGAAGAGGGTGTGAAAGATTG 146745
                                                                                           Db 146626 TCTCGGGATACCTTCTGTCCTTCCATCCTGCCCTGTACTGCCCTCTGACTCCACTGTCAC 146685
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                            CGGCTGGGAACAAACCACTAATTTGTCACTGGACTGTCTCTGGGCCTG-CTTAGACGGGG 146475
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61976 a 51605 c 50901 g 58446 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
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/chromosome="1"
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101916: gap of unknown length
150064: contig of 48148 bp in length
150164: gap of unknown length
223431: contig of 73267 bp in length
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14931: gap of unknown length
31632: contig of 16701 bp in length
31732: gap of unknown length
57782: contig of 26050 bp in length
57882: gap of unknown length
67882: gap of unknown length
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Pred. No. 3.7e-59;
                                                                                                                                                                                                                                                                          -CCCCCTTCCCATTTGTTTCTCCTTCTCTAATCCCA 146565
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                     * arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown. * This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                    Sequencing vector: plasmid; 0% (hemistry: Dye-primer ET; 100% of reads Chemistry: Dye-terminator Big Dye; 0% of reads Assembly program: Phrap; version 0.990319 consensus quality: 173282 bases at least 040 consensus quality: 178245 bases at least 030 consensus quality: 180937 bases at least 020
                                                                                                                                                                                                   Quality coverage: 3.30 in Q20 bases; agarose-fp Quality coverage: 3.64 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center project name: H_NH0341I16
Sequencing vector: M13; 1008
                                                                                                                                                                                                                                                         Insert size: 202000; agarose-fp
Insert size: 187342; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center: Washington University Genome Sequencing Center Center code: WUGSC
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On Jun 16, 2000 this sequence version replaced gi:7523957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (14-JAN-2000) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens chromosome 21 clone RP11-341I16, WORKING DRAFT SEQUENCE, 32 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Web site:http://genome.wustl.edu/gsc/index.shtml
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
                                                                                        NOTE: This is a 'working draft' sequence. It currently consists of 32 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The sequence of Homo sapiens clone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
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as soon as it is available and the accession number will
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                                                                                                                                                Location/Qualifiers
                                                     /clone="RP11-341116"
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103723: contig
103823: gap of
112141: contig
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               2146 tgagttgatcaccctgacagtgggcttcggcatcctcatcttctcccctcatcgtcaccta 2205
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clone_end:T7
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3367. .5850
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6301. .19816
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                                                                                                                                                                                /note="assembly_name:Contig45"
176745. .190442
/note="assembly_name:Contig46"
/ 33920 c 34526 g 58493 t 3
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/note="assembly_name:Contig36"
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165599. .176644
                                                                                                                                                                                                                                                                                                   /note="assembly_name:Contig43"
153668. .165498
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141656. .153567
                                                                                                                                                                                                                                                                                                                                                                          /note="assembly_name:Contig41"
129989. .141555
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120101. .129888
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/note="assembly_name:Contig38"
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    Score 256.2; DB 66; Length 190442;
    Pred. No. 1.9e-57;
    Mismatches 115; Indels 17;
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64601

83849

35110

FEATURES

3123 others

Gaps

5.

source

misc_feature misc_feature

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COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Db 104371 TGAGTTTGGCACTCTGATGGTGGGCTTTGGCATCCTCATCTTTCTCGTTGTC-ACTTATA 104313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             103955 GTTACCCACCCTCATTTGCCCTTCTCCAGGATCTCTCTTCTACTTTTTCCATTGTGCCTT 103896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    104075 CCTCTCCTCAGCTCCCGGGCCTGTCTCCCCCTTCTGCCTTTCCACCCTTTTTCCTTACCCTT 104016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            104133 GGATTAACATAAAGGAGTGGAACTGTACAAAAGAG--AGAAAGAGATAAAGGAGGCTCCT 104076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2559 gttacccaccctaatttgcccttc----aggacccttctactttttccttcctqccct 2612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2613 gtacctctctctgctcctcacccccacccctgtacccagccacct 2657
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Assembly program: XGAP4: version 4.5
Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator mid Dye; 39% of reads
Chemistry: Dye-terminator maersham; 60% of reads
Chemistry: Dye-terminator maersham; 60% of reads
Chemistry: Dye-terminator maersham; 60% of reads
Chemistry: 156012 bases at Teast Q40
Consensus quality: 160965 bases at least Q30
Consensus quality: 164137 bases at least Q20
Insert size: 167677; sum-of-contigs
Insert size: 131821; 35.2% error; agarose-fp
Quality coverage: 3.70x in Q20 bases; sum-of-contigs Quality
Coverage: 4.70x in Q20 bases; agarose-fp
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                                                                                                                                                                                                                                                                                                                                                      Center project name: dJ244G5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (13-JUN-2000) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
on Jul 16, 2000 this sequence version replaced gi:8573815.
                                                                                                                                                                                                                                                                                                                                                                                                   Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                         Web site: http://www.sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center: Sanger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center code:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pavitt, R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AL138932 170677 bp DNA
HTG 14-JUN-
HOMO Sapiens chromosome 1 clone RP1-244G5 map p11.1-13.3,
SEQUENCING IN PROGRESS ***, 31 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AL138932.10 GI:9230945
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                                                                                                                                                                                                                                                                                                                    ---- Summary Statistics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --- Genome Center
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                                                        FEATURES
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* NOTE: This is a 'working draft' sequence. It currently consists of 31 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence.
                                                                                                                                                                                                                                                     153808 154871
154872 154971:
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                                                                                                                                                                                                        156381 156480:
                                                                                           163850 163949:
                                                                                                                                                 60085 160184:
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11646 11745: gap of 100 bp
11746 13929: contig of 2184 bp in length
13930 14029: gap of 100 bp
14030 16875: contig of 2846 bp in length
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Location/Qualifiers
1. .170677
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70447: gap of 100 bp
77556: contig of 7109 bp in length
77656: gap of 100 bp
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                                                   170677: contig of 6728
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                                                                                                 0184: gap of 100 b
163849: contig of 3665
                                                                                                                                                                             160084: cont
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                                                                                                                                                                                                                                                                              33807: gap of 100 b
154871: contig of 1064
                                                                                                                                                                                                                                                                                                                                                                                                                                                           13272: gap of 100 bp
150964: contig of 7692 bp
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141779: contig of 1325 bp
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140354: contig of 19709 bp in length
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31: contig of 3569 bp in length
gap of 100 bp
55: contig of 5064 bp in length
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contig of 2846 bp in length
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/organism="Homo sapiens"

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20489. .2
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49658. .51777
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fragment_chain:2"
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REFERENCE
AUTHORS
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Best Local Similarity
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Assembly program: XGAPA; version 4.5 sequencing vector: plasmid; L08752; 100% of reads Chemistry: Dye-terminator Blg Dye; 100% of reads consensus quality: 112851 bases at least Q40 Consensus quality: 127377 bases at least Q30 Consensus quality: 136503 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AL391417 148540 bp DNA HTG 24-JAN-2001
Homo sapiens chromosome 6 clone RP11-15J23, *** SEQUENCING IN
PROGRESS ***, 45 unordered pieces.
                                                                                                                                                                                                                                                            Submitted (21-JAN 2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clope requests: clonerequest@sanger.ac.uk on Aug 29, 2000 this sequence version replaced gi:9931024.
                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homoli, (bases 1 to 148540)
                                                                                                                                                         Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
-----Project Information
                                                                                                                                                                                                                           Center: Sanger Centre
                                                                                                                                                                                                                                                                                                                                        Direct Submission
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                                                                                                                                  Center project name: bA15J23
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151065. .152556
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160185. .163849
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152657...153707
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    Project Information

                                                                                                                Summary Statistics
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Pred. No. 5.5e-46;
                                                                                   100% of reads
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Insert size: 144140; sum-of-contigs
Insert size: 165039; 32.7% error; agarose-fp
Quality coverage: 1.71x in Q20 bases; sum-of-contigs Quality
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NOTE: This is a 'working draft' sequence. It currently consists of 45 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 55969 56068: gap of 100 bp

56069 59340: contig of 3272 bp

59341 59440: gap of 100 bp

59441 61462: contig of 2022 bp

61463 61562: gap of 100 bp

61563 63584: contig of 2022 bp
                           101834 101933: gap of 100 bp
101934 104031: contig of 2098 bp in length
                                                                                                  97305 97404:
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95017 973
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19572: 19671: gap of 100 bp
19672: 21869: contig of 2198 bp in length
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3178 5415: con
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1059 30798; gap of 100 bp
1799 33751; contig of 2953 bp
1752 33851; gap of 100 bp
1752 36057; contig of 2265
18 36157; gap of 100 bp
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. gap of 2206 bp in length

100 bp

100 bp

100 bp in length

100 bp

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45601: gap of 100 bp
47671: contil of 2070 bp
72 47771: gap of 100 bp
72 50828: contig of 3057 bp
73 50928: gap of 100 bp
74 50928: gap of 2022 bp
75 50928: gap of 100 bp
76 50928: gap of 100 bp
             104131: gap of
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                                                                      404: gap of 100 bp
101833: contig of 4429 bp in length
                                                                                                                                                        218: gap of 100 bp
91581: contig of 5363 bp in length
581: gap of 100 bp
94916: contig of 3235 bp in length
                                                                                                                                                                                                                                                                                                                                                                              νο: gap of
68895: con+
                                                                                                               )16: gap of 100 bp
97304: contig of 2288 bp in
                                                                                                                                                                                                                                      86118: contig of 5927 b
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8529: con
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9: gap of 100 bp
10965: contig of 2336 bp in length
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27: contig of 2758 b
gap of 100
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70: contig of 4805 bp in length
gap of 100 bp
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contig of 2121 k
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contig of 2238 bp in length
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f 5871 bp in length
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f 3601 bp in length
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145771 145870: g
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21811 121910: מפ
פיים מחור
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .32511 132610:
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56069. .59340
/note="assembly_fragment:00328"
59441. .61462
                                                                                  /note="assembly_fragment:00320'53231...55968"
                                                                                                                                                                    /note="assembly_fragment:00302"
47772. .50828
                                                                                                                                                                                                                                                               43384.
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                                                        'note="assembly_fragment:00321"
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/db_xref="taxon:9606"
/chromosome="6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note="assembly_fragment:00178"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="assembly_fragment:00020"
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128837: cc<sup>-</sup>
1937
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148540: contig of 2670 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7665: gap of 100 bp 140029: contig of 2364 bp in length
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137565: contig of 2048
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135417: cont
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119288: contig of
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109230: cont
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143581: cont
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.13704: contig of
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contig of 2171 bp
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VERSION
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KEYWORDS
                             ACCESSION
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Local Similarity 72.9%;
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                                                         Human DNA sequence from clone RP11-43916 on chromosome
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              AL445926.5 GI:12329473
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76303. .80091
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63685. .65805
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61563. .63584
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101934. .104031
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                                                                             167253 bp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 180.8; DB Pred. No. 3.7e-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 148540;
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Db 102334 CCTTTTCTGTCTTTCCTCCTATTTCCTCCTTCT--CCTACCCCTGCTAGATACTGGG
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                                                                                              Db 102572 CAGAATCAAACTATGTACAATGAACCTCTGAGGAGGAAGACAGGGGTGATTGCTGGGCT$
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Best Local Similarity 72.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2461 cottteccatcaeccettecccatttectettecttetetaeteatgccagattttggg
2740 agoctactgtcccttcccactgtcctttctccaggccctcagatggcacattagggtgg
                                                                                                                                                                                                                                                                                                                                                                                                                              2691 cagggtcaaac----tacattgagcccctgagga-----caggggcatctctgggc
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On Jan 21, 2001 this sequence version replaced gi:12214354.

On Jan 21, 2001 this sequence version replaced gi:12214354.

On Jan 21, 2001 this sequence version replaced gi:12214354.

On Jan 21, 2001 this sequence version replaced gi:12214354.

Where differences are found these are annotated as variations

together with a note of the overlapping clone name. Note that the

variation annotation may not be found in the sequence submitssion

corresponding to the overlapping clone, as we submit sequences with

only a small overlap as described above.

This sequence has been finished according to sequence map criteria

as follows. An attempt is made to resolve all sequencing problems,

as follows. An attempt is made to resolve all sequencing problems,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       such as compressions and repeats, but not necessarily within known annotated repeat sequence elements. Where the sequence is ambiguous, there is an annotation using the 'unsure' feature key. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:
Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (20-JAN-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          was generated from part of bacterial clone contigs or numeric chromosome 9, constructed by the Sanger Centre Chromosome Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr9
RP11-43916 is from the library RPCI-11.2 constructed by the of Pieter de Jong. For further details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           http://www.sanger.ac.uk/Projects/C_elegans/wormpep This spquence was generated from part of bacterial clone contigs of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VECTOR: pBACe3.6
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/clone_lib="RPCI-11.2"
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/chromosome="9"
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Pred. No. 3.7e-37;
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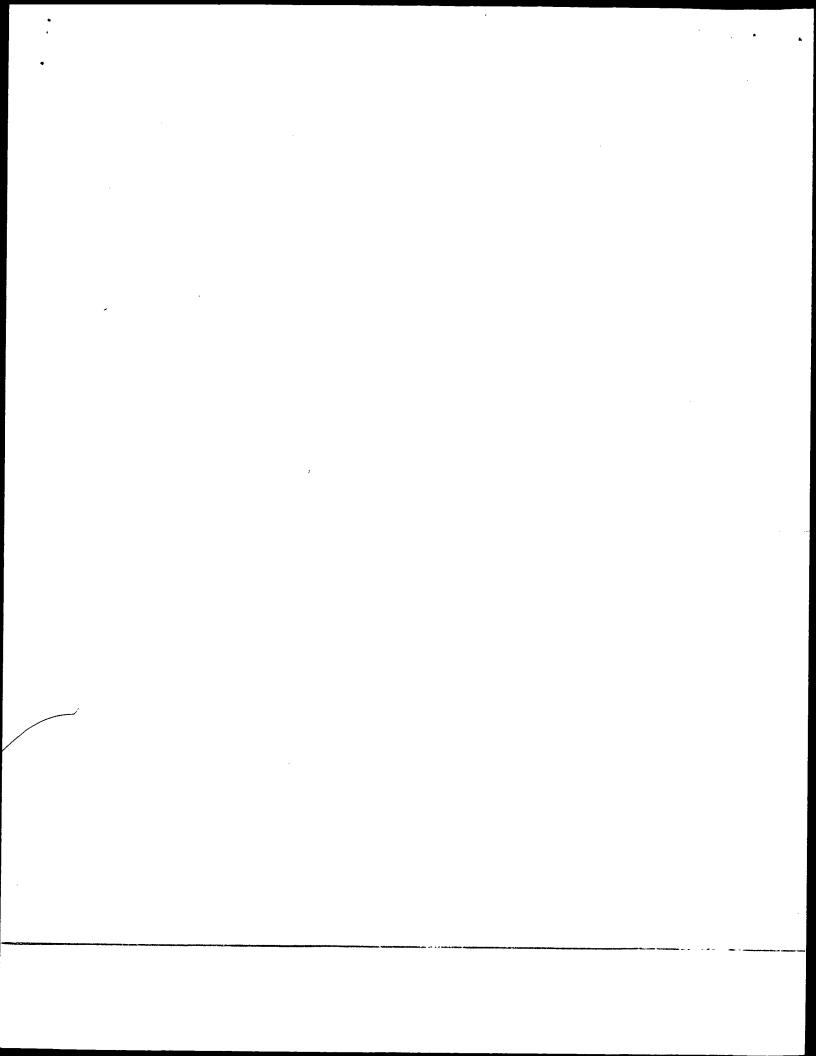
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FEATURES
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AL590397/c
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                                                                                                                               source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Assembly program: XGAP4; version 4.5 Sequencing vector: plasmid; L08752; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Consensus quality: 167948 bases at least Q40 Consensus quality: 168125 bases at least Q30 Consensus quality: 168249 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Insert size: 168337; sum-of-contigs
Insert size: 160691; 19.0% error; agarose-fp
Quality coverage: 9.38x in Q20 bases; sum-of-contigs Quality
coverage: 9.83x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (12-APR-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Apr 12, 2001 this sequence version replaced gi:13568355.
                                                                                                                                                                                                                                                                                                         NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Web site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center: Sanger Centre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AL590397 168537 bp DNA HTG HOMO Sapiens chromosome 9 clone RP11-376021, PROGRESS ***, 3 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                         61919 62018: gap of 62019 168537: cont
                                                                                                                                                                                                           1 6100: contig of 6100 bp in length 6101 6200; gap of 100 bp 6201 61918: contig of 55718 bp in length
                                            /organism="Homo sapiens"
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/chromosome="9"
/clone="RP11-376021"
/clone_lib="RPCI-11.2"
                                                                                                                                            ocation/Qualifiers
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http://www.sanger.ac.uk
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Search completed: June 27, 2001, 17:23:44 Job time: 10068 sec

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Db 122768 TACTGAGTTTTATTAAAATATA 122747
                                                                                                                            Db 122881 GTGTGCTGCCGGGTGGGCATCCCACCTCCAGCCCACAGTGTTCAGTTTCACTTTTTAGT 122822
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                                                                                                                                                                                                                                                                   Db 122998 CAGAATCAAACTATGTACAATGAACCTCTGAGGAGGAAGACAGGGGTGATTGCTGGGCT
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                2919 taatgagtttcattaaaataga 2940
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1 31342 c 32090 g
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/note="assembly_fragment:00055
fragment_chain:1
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clone_end:T7
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fragment_chain:1"
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Page 23



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Mouse PAMP coding
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Human secreted pro
EST sequence #2.
EST sequence #4.
EST sequence #4.
Human brain Expres
EST sequence #5.
EST sequence #1.
EST clone BB54. H
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| | brane protein; immunogen; disease; Lewy body variant; neuropsychiatric disease; oss; developmental disorder; | uman PKD gene. uman pKD gene. uman pKD locus uman pKD locus uman pKD locus ntre ply genom 815A antigen pl AGE genomic DNA. IA genomic DNA. IA genomic con 114 genomic con 115 | EST sequence #6. EST sequence #7. D. melanogaster PA |

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St George-Hyslop PH,
                                            2000-665001/64.
)B; AAY97549.
                                                  Fraser PE;
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Isolated presentlin associated membrane proteins and nucleic acids encoding them, useful for investigating and diagnosing Alzheimer's disease and other neurodegenerative diseases -

Claim 8; Page 67-68; 79pp; English.

diseases (e.g. Alzheimer's disease, Levy body variant, Parkinson's disease-dementia complex), neuropsychiatric diseases (e.g. schizophrenia, age-associated memory loss), developmental disorders, and neoplasms. These may further be used to deduce the structural organisation and topology of PAMP, to identify proteins which interact with PAMP either in concert with presenilin 1 (PSI) and PS2, or independently, and to create cell-free systems, transfected cell lines, and animal modes of This sequence encodes the human presentilin associated membrane protein (PAMP) of the invention. PAMP polypeptides may be used as an immunogen generate antibodies that recognise the PAMP polypeptide. The PAMP nucleotide and protein sequence may also be used for diagnosing individuals who are at risk or who have a variety of neurodegenerative neurodegenerative and other diseases. 1mmunogen to

Sequence 2949 BP; 682 A; 803 C; 692 G; 770 T; 2 other;

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| ۵ N | 621 gctgggacgtgctctgtatgagcttqcaqqaqqaaccaacttcagcgacacacattcagcacacacacacaca | Qy |
| 62 | 1561 tgaagaggacctgaactttgtaacagacactgccaaggccctggcagatgtggccacggt 1 | p d |
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| ວ ວ | 321 ggtggaggatctcctqqccacattqqaqaqaaqaqtqqtqqtqqtqqtqctqtacggaacca | Qy |
| 1320 | 1261 attagagctttggatgcacacagatcctgtttctcagaaaaatgagtctgtacggaacca | P 04 |
| 1260 | 01 cgtgcagttagagaatgttgactcatttgtggagctgggacaggtggccttaagaactt | Db |
| 26 | 01 cgtgcagttagagaatgttgactcatttgtggagctgggacaggtggccttaagaacttc | Qy |
| 20 | 41 aacttttgactacattggcagctcgaggatggtctacgatatggagaagggcaagtttcc | Db |
| 20 | 41 aacttttgactacattggcagctcgaggatggtctacgatatggagaagggcaagtttcc | Qy |
| 14 | 1081 aaaggcacctgatgtgaccaccctgccccgcaatgtcatgtttgtcttctttcaaqqqq | Db |
| 14 | aaggcacctgatgtgaccaccctgccccgcaatgtcatgtttqtctttctttcaagggg | Qy |
| 80 | 11111111111111111111111111111111111111 | Db |
| 08 | | Qy |
| 20 1 | 961 cagggttgtggttgctgccacccggctggatagtcgttcctttttctggaatgtggccc | Db |
| o | 61 cagggttgtggttgctgccacccqqctqqataqtcqttcctttttctqqaaatqtqqqc | QУ |
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|) | agctccatccaaagcaccttcagcatcaacccagaaatcqtctqtqacccctqtrtq | Qy |
| - 4 | 781 tgccatgcagctcttttcacacatgcatgctgtcatcagcactgccacctgcatgqqch | Дb |
| • | gccatgcagctcttttcacacatgcatgctgtcatcagcactgccacctgcatgcggg | Qy |
| | 721 gcagtgctatcaagatcacaacctgagtcagaatggctcagcaccaacctttcccactata | DЬ |
| ρō t | cagtgctatcaagatcacaacctgagtcagaatggctcagcaccaaccttrccaactat | Qy |
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Isolated presentlin associated membrane proteins and nucleic action encoding them, useful for investigating and diagnosing Alzheimer disease and other neurodegenerative diseases

9; Page 70-71; 79pp; English.

This sequence encodes the mouse presentilin associated membrane protein (PAMP) of the invention. PAMP polypeptides may be used as an immunogen generate antibodies that recognise the PAMP polypeptide. The PAMP nucleotide and protein sequence may also be used for diagnosing individuals who are at risk or who have a variety of neurodegenerative diseases (e.g. Alzheimer's disease. Levy body variant, Parkinson's disease-dementia complex), neuropsychiatric diseases (e.g. schizphreni age-associated memory loss), developmental disorders, and neoplasms. These may further be used to deduce the structural organisation and topology of PAMP, to identify proteins which interact with PAMP either in concert with presentlin 1 (PS1) and PS2, or independently, and to create cell-free systems, transfected cell lines, and animal modes of neurodegenerative and other diseases. phrenia, ç

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                                                                                                                          The present sequence represents a human expressed sequence tag (EST). The polynucleotide, which is a secreted EST, and the encoded protein are predicted to have useful biological activities which would make them suitable for treating, preventing or ameliorating medical conditions in humans and animals, although no supporting data is given. Suggested activities include nutritional activity, immune stimulating or suppressing activity, haematopoiesis regulating activity, tissue growth activity, haematopiesis regulating chemotactic/chemokinetic activity, activin/inhibin activity, cadherin/tumour invasion suppressor activity, tumour inhibition activity. The polynucleotide may also be useful for gene therapy.
                                                                                                                                                                                                                                                                                                                                              New polynucleotides encoding human secreted proteins - derived from e.g. human blood, kidney, foetal lung, placenta, testes, brain, ovary, pituitary, retina and colon cDNA libraries.
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gene therapy; c
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                                                     Dumas Milne Edwards J,
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Best Local
PAMP; presenilin associated membrane protein; immunogen;
                                         EST sequence #2.
                                                                              12-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence is one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins An ORF has been identified within the sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA; of the mRNA because they are well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain nastream remniatory semences and to design appreciation.
                                                                                                                                                     AAA37890 standard; DNA; 473
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 473 BP; 129 A; 116 C; 117 G; 111 T; 0 other;
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                  ctagtgtacagtgcccaaatgatgggtttggtgtttactccaattcctatgggccagag
                                                                                                                    gtagaatcgctggtcttgccgtgactctagccaagcccaactcaacttcaagcttctct
                                                                                                                                                                                      gccgaattgctggtcttgcagtgtccttgaccaagcccagtcctgcctcaggcttctctc
                                                                                                                                                                                                                                                                                                ttctgctggagagcaagcaattttaccagggatttaatggagaagctgaaagggagaacca
                                                                                                                                                                                                                                                                                                                                                                                                         tggagaaagaagaacctgaagtgggtgttgaccgatggccccaaccccccttacatgg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ccactcatcagattggctgccagtcttcaattagtggagacacagggggttatccacgtag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tggagaggaagatatatatccccttaaataaaacagctccctgtgttcgcctgctcaacg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ccactcatcagattggctgccagtcttcaattagtggggatacaggggttatccatgta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     401;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99US-0127452
99US-0173826
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Pred. No. 2.9e-89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
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301

ctagtgtgcagtgcccaaatgatgggtttggtaattactccaactcctacgggccagag

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RESULT
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                Qy
                                                 Matches 399; Conser
                                                                                                                                                                              This sequence represents an expressed sequence tag used to isolate the human presenilin associated membrane protein (PAMP) coding sequences of the invention. PAMP polypeptides may be used as an immunogen to generate antibodies that recognize the PAMP polypeptide. The PAMP nucleotide and protein sequence may also be used for diagnosing individuals who are at risk or who have a variety of neurodegenerative diseases (e.g. Alzheimer's disease, Lewy body variant, Parkinson's disease-dementia complex), neuropsychiatric diseases (e.g. schizophrenia, age-associated memory loss), developmental disorders, and neoplasms. These may further be used to deduce the structural organisation and topology of PAMP, to identify proteins which interact with PAMP either in concert with presenilin 1 (PS1) and PS2, or independently, and to create cell-tree systems, transfected cell lines, and animal modes of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PAMP; presentiin associated membrane protein; immunogen; neurodegenerative disease; Alzheimer's disease; Lewy body variant; Parkinson's disease-dementia complex; neuropsychiatric disease; schizophrenia; age-associated memory loss; developmental disorder; neoplasm; diagnosis; EST; expressed sequence tag; ds.
                 1437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAA37891 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Isolated presentlin associated membrane proteins and nucleic acids encoding them, useful for investigating and diagnosing Alzheimer's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-665001/64.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-APR-1999;
30-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      03-APR-2000; 2000WO-CA00354.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-FEB-2001
                                                                                                                                   Sequence 463
                                                                                                                                                                                                                                                                                                                                                                                                                               Example 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                disease and other neurodegenerative diseases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (UTOR ) UNIV TORONTO GOVERNING COUNCIL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     421
                                                                                                                                                                       neurodegenerative and other diseases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ttagtttccccatctttcttcttgaagatgaaaatgaaaccaaagtcatcaag 721
gagotogaaacatototggogttgttotggotgaccactotggtgcottccataacaaat 1496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ttgctcactggaagaaaacactgtggaatgaactcggcaaaggcttggcttatgaagacc
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                                                                                                                                                                                                                                                                                                                                                                                                                               Page 60; 79pp; English.
                                                   Conservative
                                                                                                                                     B₽;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99US-0127452.
99US-0173826.
                                                                                                                                     113 A; 134 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA;
                                                                11.9%;
86.2%;
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                                                   0;
                                                                 Score 350.2; DB 2
Pred. No. 3.7e-87;
                                                                                                                                     113 G; 103 T; 0 other;
                                                   Mismatches
                                                                                   DB 21;
                                                   63;
                                                   Indels
                                                                                   Length 463;
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RESULT
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1677
                                                                                                                                                                                                                                                                                                                                                                                                                          PAMP; presentiin associated membrane protein; immunogen; neurodegenerative disease; Alzheimer's disease; Lewy body varian; Parkinson's disease-dementia complex; neuropsychiatric disease; schizophrenia; age-associated memory loss; developmental disorde; neoplasm; diagnosis; EST; expressed sequence tag; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1797
                                                                                         Isolated presentiin associated membrane proteins and nucleic acids encoding them, useful for investigating and diagnosing Alzheimer's disease and other neurodegenerative diseases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAA37892 standard; DNA; 481 BP.
                                                                                                                                                                                     St George-Hyslop PH,
                                                                                                                                                                                                                                                     01-APR-1999;
30-DEC-1999;
                                                                                                                                                                                                                                                                                                   03-APR-2000; 2000WO-CA00354
                                                                                                                                                                                                                                                                                                                                                                                                 Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EST sequence #4:
                                                            Example 1; Page 61; 79pp; English.
                                                                                                                                                                                                                                                                                                                                                                  WO200060069-A1
                                                                                                                                                          WPI; 2000-665001/64
                                                                                                                                                                                                                      (UTOR ) UNIV TORONTO GOVERNING COUNCIL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             attaccagagtatttacgacactgctgagaacattaatgtgagctatcccgaatggctga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                attaccagagcatttatgacacggctgagaacattaatgtgacctatcctgagtggca
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                caaacctgactgggcaaggcgaccaacctcacccgagagcagt 463
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          catggtttcagtcgatcctgaaacatgacctaaggtcctatttggatgacaggcctcttc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         catggttccagtctatcctcaggcaggacctaaggtcctacttgggtgacgggcctctt
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         aggctgatccccaaacggttacccgcctgctctatgggttcctgattaaagccaacaact
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cagtgctggcgcgtgcactgtatgagcttgcaggaggaaccaacttcagcagctccatcp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                     99US-0173826
                                                                                                                                                                                                                                                                      99US-0127452
                                                                                                                                                                                                                                                                                                                                                                                                                                            developmental disorder;
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This sequence represents an expressed sequence tag used to isolate the human presentlin associated membrane protein (PAMP) coding sequences of the invention. PAMP polypeptides may be used as an immunogen to

PAMP polypeptides may be used

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RESULT
AAQOOD
XX AAQO
XX AAQO
XX AAQO
XX Huma
DT 16-b
DT 16-b
XX U
BEN Huma
XX Gene
XX Gene
XX Gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          generate antibodies that recognise the PAMP polypeptide. The PAMP nucleotide and protein sequence may also be used for diagnosing individuals who are at risk or who have a variety of neurodegenerative diseases (e.g. Alzheimer's disease, Levy body variant, Parkinson's disease-dementia complex), neuropsychiatric diseases (e.g. schizophrenia, age-associated memory loss), developmential disorders, and neoplasms. These may further be used to deduce the structural organisation and topology of PAMP, to identify proteins which interact with PAMP either in concert with presentlin 1 (PSI) and PS2, or independently, and to create cell-free systems, transfected cell lines, and animal modes of neurodegenerative and other diseases.
                  12-FEB-1993;
                                                     19-AUG-1993.
                                                                                       WO9316178-A.
                                                                                                                      Homo sapiens.
                                                                                                                                                           transcription;
                                                                                                                                                                          Gene transcription product;
                                                                                                                                                                                                         Human brain Expressed Sequence Tag EST01062.
                                                                                                                                                                                                                                                  16-MAR-1994
                                                                                                                                                                                                                                                                                                                     AAQ60994 standard; DNA; 328
                                                                                                                                                                                                                                                                                                                                                                                                                           1985 gaccgactcccccggtgtgtgcgttc 2010
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 481 BP; 121 A; 135 C; 121 G; 104 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                              421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                361
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               actggcaaggcgaccaacctcacccgagagcagtgccaggatccaagtaaagtcccaaat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gagagcaaggatttatatgaatactcgtgggtacaaggcccttggaattccaacaggaca 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gaaaacaaggatctgtatgagtactcatgggtccagggccctttgcattctaatgagacg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    atcgccgtctccagccctaccaacacgacttacgttgtgcagtacgccttggcaaacctg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      atcgctgtctccagccccaccaacaccacttatgttgtacagtatgccttggcaaatttg 1864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cagtctatcctcaggcaggacctaaggtcctacttgggtgacgggcctcttcaacattac 1804
                                                                                                                                                                                                                                                                                                                                                                                                          gagaggctcccacagtgtgtgcgctc 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ccccagacagttacacgtctgctctatgggttcctggttagagctaacaactcatggttt 180
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                                                                                                                                                                                                                                                (first entry)
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                                                                                                                                                         mapping; locations; chromosomes; chromosomal; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11.4%;
                                                                                                                                                                          genetic markers; tagging; in vivo;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 337.2; DB 2
Pred. No. 1.5e-83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches 68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 21;
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                                                                                                                                                                                                                                                                                                                                                                                   1657
                                              PAMP; presentiln associated membrane protein; immunogen; neurodegenerative disease; Alzheimer's disease; Lewy body variant; Parkinson's disease-dementia complex; neuropsychiatric disease; schizophrenia; age-associated memory loss; developmental disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1357 tgctggtgtccctgctgtcatcctcaggaggccaaatcagtcccagcctctcccaccatc 1416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The Expressed Sequence Tag was isolated from a human brain cDNA I library as part of a large set of ESTS which can be used as markers for human genes transcribed in vivo. They can be used to facilitate tagging of most human genes, for mapping locations of expressed gene on chromosomes, for individual or forensic identification, for mappi locations of disease-associated genes, for identification of tisbue type, and for prepn. of antisense sequences, probes and constructs. EST01062 has an "excellent" coding probability as evaluated using the
                                  neoplasm; diagnosis; EST; expressed sequence tag;
                                                                                                                                          EST sequence #5
                                                                                                                                                                                 12-FEB-2001
                                                                                                                                                                                                                                                        AAA37893 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Enriched oligonucleotides and corresp. sequences - used as markers for human genes transcribed in-vivo, facilitate tagging of most human genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 328 BP; 75 A; 93 C; 80 G; 80 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   coding-region prediction program CRM. See also AAQ59041-Q61440.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 4; Page 423; 500pp; English
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                                                                                                                                                                                                                                                                                                                                                  301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 tgctggtgtccctgctgtcatcctcaggaggccaaatcagtcccagcctctcccaccat
                                                                                                                                                                                                                                                                                                                                              caacttcagcgacacagttcaggctgat 328
                                                                                                                                                                                                                                                                                                                                                                  caacttcagcgacacagttcaggctgat 1684
                                                                                                                                                                                                                                                                                                                                                                                                                                       ggccctggcagatgtggccacggtgctgggacgtgctctgtatgagcttgcaggaggaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tggtgccttccataacaaatattaccagagtatttacgacactgctgagaacattaatgt 1536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ttccctgcagcgatttcttcgagctcgaaacatctctggcgttgttctggctgaccactc 1476
                                                                                                                                                                                                                                                                                                                                                                                                                    ggccctggcagatgtggccacggtgctgggacgtgctctgtatgagcttgcaggaggaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gagctatcccgaatggctgagccctgaagaggacctgaactttgtaacagacactgcc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11.1%; Score 328; DB 14;
100.0%; Pred. No. 4.4e-81
vative 0; Mismatches (
                                                                                                                                                                                                                                                        DNA;
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Best Local Similarity 83.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This sequence represents an expressed sequence tag used to isolate the human presentlin associated membrane protein (PAMP) coding sequences of the invention. PAMP polypeptides may be used as an immunogen to generate antibodies that recognist the PAMP polypeptide. The PAMP nucleotide and protein sequence may also be used for diagnosing nidividuals who are at risk or who have a variety of neurodegenerative diseases (e.g. Alzheimer's disease, Lewy body variant, Parkinson's diseases dementia complex), neuropsychiatric diseases (e.g. schizophrenia, age-associated memory loss), developmental disorders, and neoplasms. These may further be used to deduce the structural organisation and topology of PAMP, to identify proteins which interact with PAMP either in concert with presenilin 1 (PS1) and PS2, or independently, and to create cell-free systems, transfected cell lines, and animal modes of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-DEC-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    St George-Hyslop PH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (UTOR ) UNIV TORONTO GOVERNING COUNCIL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 1; Page 61; 79pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Isolated presentiin associated membrane proteins and nucleic acids encoding them, useful for investigating and diagnosing Alzheimer's
                                                                                                                                                                                                                                                                                                                                                                                                  1784 gacgggcctcttcaacattacatcgctgtctccagccccaccaacaccacttatgttgta 1843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 398 BP; 107 A; 111 C; 99 G; 81 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              neurodegenerative and other diseases.
                                                                                            2024 gccagggccttgtctcctgcctttgaactgagtcagtggagctctactgaatactctaca 2083
                                                                                                                                                                                                                              179
                                                                                                                                                                                                                                                                                                                                                                                60
                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 agagctaaccactcatggtttcagtcgatcttgaaacatgacctaagg-cctatttggat 59
                                                                                                                                                                                                                                                                                                                       cagtatgccttggcaaatttgactggcacagtggtcaacctcacccgagagcagtgccag 1903
                                                                                                                                                                           gacaggcctcttcaacactacatcgccgtctccagccctaccaacacgacttacgttgtg 119
                                                                                                                                                                                                                            gatccaagtaaagtcccaaatgagagcaaggatttatatgaatactcgtgggtacaaggc
                                                                                                                                                                                                                                                cagtacgccttgg-aaacctgactggcaaggcgaccaacctcacccgagagcagtgccag 178
                 tggactgagagccgctggaaagatatccgtgcccggatat 2123
                                                                                                                                                   ccttggaattccaacaggacagaggctcccacagtgtgtgcgctccacagtgcgactg
tgggcggagagccgctggaaagacatccaagctcggatat 398
                                                                            gccagggccttgtcccctgcctttgaactgagtcagtggagctccacagaatactctacg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and other neurodegenerative diseases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99US-0127452
99US-0173826
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 Mismatches

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 273.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 21; Length 398;
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                                                                                                                                                                                                                                               Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAA37889;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAA37889 standard; DNA; 422 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EST sequence #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence represents an expressed sequence tag used to isolate the human presenilin associated membrane protein (PAMP) coding sequences of the invention. PAMP polypeptides may be used as an immunogen to generate antibodies that recognise the PAMP polypeptide. The PAMP nucleotide and protein sequence may also be used for diagnosing individuals who are at risk or who have a variety of neurodegenerative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-APR-1999;
30-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               neoplasm; diagnosis; EST; expressed sequence tag; ds.
                                                                                                                                                                                                                                                                                                                                                                   diseases (e.g. Alzheimer's disease, Lewy body variant, Parkinson's disease-dementia complex), neuropsychiatric diseases (e.g. schizophrenia, age-associated memory loss), developmental disorders, and neoplasms. These may further be used to deduce the structural organisation and topology of PAMP, to identify proteins which interact with PAMP either in concert with presenilin 1 (PS1) and PS2, or independently, and to create cell-free systems, transfected cell lines, and animal modes of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              St George-Hyslop PH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              03-APR-2000; 2000WO-CA00354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             disease and other neurodegenerative diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Isolated presentlin associated membrane proteins and nucleic acids encoding them, useful for investigating and diagnosing Alzheimen's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-665001/64.
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                                                                                                                                                                                                                                                                                                                    Sequence 422 BP; 100 A; 92 C; 124 G; 106 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 1; Page 59; 79pp; English.
                                                                                                                                                                                                                                                                                                                                                       neurodegenerative and other diseases.
                                                                                                                                                                 126 ctcagcagagaggcaagatggctacggcagggggtggctctggggctgacccggggaagtc 185
                                                                                                                                                  1 cccagcggagaggcaagatggctacgactaggggcggctctgggcctgacccaggaagtc
                                                                                          ggggtctccttcgccttctgtctttctgcgtcctactagcaggtttgtgcaggggaaact 245
                 cagtggagaggaagatatatatccccttaaataaaacagctccctgtgttcgcctgctca
                                                                       ggggtcttctt---cttctgtctttttccgtggtactggcaggattgtgtgggggaaact
cagtggagaggaaaatctacattcccttaaataaaacagctccttgtgtccgcctgctca
                                                                                                                                                                                                                             283;
                                                                                                                                                                                                                           Conservative
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99US-0173826.
                                                                                                                                                                                                                                               7.18;
80.68;
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                                                                                                                                                                                                                             Score 208.2; DB Pred. No. 9e-48; 0; Mismatches
                                                                                                                                                                                                                                                                  DB 21; Length 422;
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RESULT 1
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                                                   treating, preventing or ameliorating medical conditions in humans and animals, although no supporting_data is given. Suggested activities include nutritional activity, immune stimulating or suppressing activity, haematopoisesis regulating activity, tissue growth activity, activity, activity, hemotactic/chemokinetic activity, haemostatic and thrombolytic activity, receptor/ligand activity, anti-inflammatory activity, cadherin/tumour invasion suppressor activity, tumour inhibition
                                                                                                                                                                             This sequence represents an expressed sequence tag (EST), and is a polynucleotide of the invention. The polynucleotides of the invention are all secreted EST sequences isolated from a variety of human tissue sources. The EST sequences and proteins encoded by them are predicted to have useful biological activities which would make them suitable for
                                                                                                                                                                                                                                                                                                                    New polynucleotides encoding human secreted proteins - derived from e.g. human blood, kidney, foetal lung, placenta, testes, brain, ovary, pituitary, retina and colon cDNA libraries
                                               activity.
                                                                                                                                                                                                                                                                                           Claim 1; Page 361; 633pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1999-070076/06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Expressed sequence tag; secreted protein; haematopoiesis regulator; tissue growth; activin; inhibin; tumour invasion suppressor; EST; h chemotaxis; chemokinesis; haemostasis; gene therapy; thrombolysis; receptor; ligand; anti-inflammatory; tumour inhibitor; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (GEMY ) GENETICS INST INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-OCT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAV86828;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                297 gtctgctggagggaag-----tcttcacagagatgtaatggagaagctga 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           426
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tagtagaagaagaggacctacagtgggtattgactgatggccccaaccccccttaca 425
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   acgccactcatcagattggctgccagtcttcaattagtggagacacaggggttatccacg 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tagtggagaaagaagaaga.ctgaagtgggtgttgacgatggccccaacccccttacatg
                                          The EST sequences are also stated to be useful
                                                                                                                                                                                                                                                                                                                                                                                                                              Spaulding V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97us-0835913.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98WO-US06954.
                                                                                                                                                                                                                                                                                                                                                                                                                                Lavallie ER, McCoy JM, Treacy M;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Merberg D;
                                        for gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      human;
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Matches 187; Conserv

nilarity 100.0%; I Conservative 0;

6.3%; Score 187; DB 20 100.0%; Pred. No. 5e-42;

DB 20; 0;

Length 247; Indels

0;

Gaps

0

Sequence 172 BP; 37 A; 46 C;

50 G;

39 T; 0 other;

Query Match

Sequence 247 BP; 62 A; 60 C; 53 G; 72 T; 0 other;

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RESULT 12
AAA37894
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                 human presentiin associated membrane protein (PAMP) coding sequences of the invention. PAMP polypeptides may be used as an immunogen to generate antibodies that recognise the PAMP polypeptide. The PAMP nucleotide and protein sequence may also be used for diagnosing individuals who are at risk or who have a variety of neurodegenerative diseases (e.g. Alzheimer's disease, Lewy body variant, Parkinson's disease dementia complex), neuropsychiatric diseases (e.g. Schizophrenia, Phese may further be used to deduce the structural organisation and topology of PAMP, to identify proteins which interact with PAMP either in concert with presentlin 1 (PSI) and PS2, or independently, and to create cell-free systems, transfected cell lines, and animal modes of neurodegenerative and other diseases.
                                                                                                                                                                                                                                                                                                     Isolated presenilin associated membrane proteins and nucleic acids encoding them, useful for investigating and diagnosing Alzheimer's disease and other neurodegenerative diseases
                                                                                                                                                                                                                                       This sequence represents an expressed sequence tag used to isolate the
                                                                                                                                                                                                                                                                          Example 1; Page 61-62; 79pp; English.
                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-665001/64.
                                                                                                                                                                                                                                                                                                                                                                                                            St George-Hyslop PH,
                                                                                                                                                                                                                                                                                                                                                                                                                                          (UTOR ) UNIV TORONTO GOVERNING COUNCIL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         03-APR-2000; 2000WO-CA00354.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PAMP; presentiin associated membrane protein; immunogen; neurodegenerative disease; Alzheimer's disease; Lewy body variant; Parkinson's disease-dementia complex; neuropsychiatric disease; schizophrenia; age-associated memory loss; developmental disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200060069-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAA37894 standard; DNA; 172 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    neoplasm; diagnosis; EST; expressed sequence tag; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12-FEB-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       176 gaaaatgaaaccaaagtcatcaagcagtgctatcaagatcacaacctgagtcagaatgg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          698 gaaaatgaaaccaaagtcatcaagcagtgctatcaagatcacaacctgagtcagaatggc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  236 tcagcac 242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tcagcac 764
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99US-0173826.
                                                                                                                                                                                                                                                                                                                                                                                                            Fraser PE;
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AAA37895/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2002 tgtgcgttctactgcacgattagccagggccttgtctcctgcctttgaactgagtcagtg 2061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2122 atttctcatcgccagcaaagagcttgagttgatcaccctgacagtgggcttc 2173
                                             This sequence represents an expressed sequence tag used to isolate the human presenilin associated membrane protein (PAMP) coding sequences of the invention. PAMP polypeptides may be used as an immunogen to generate antibodies that recognise the PAMP polypeptide. The PAMP nucleotide and protein sequence may also be used for diagnosing individuals who are at risk or who have a variety of neurodegenerative diseases (e.g. Alzheimer's disease, Lewy body variant, Parkinson's diseases (e.g. achizophrenia, neuropsychiatric diseases (e.g. schizophrenia, age-associated memory loss), developmental disorders, and neoplasms. The sease may further be used to deduce the structural organisation and topology of PAMP, to identify proteins which interact with PAMP either in concert with presentlin 1 (PSI) and PS2, or independently, and to create cell-free systems, transfected cell lines, and animal modes of neurodegenerative and other diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PAMP; presentiin associated membrane protein; immunogen; neurodegenerative disease; Alzheimer's disease; Lewy body variant; parkinson's disease-dementia complex; neuropsychiatric disease; schizophrenia; age-associated memory loss; developmental disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAA37895 standard; DNA; 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EST sequence #7.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   03-APR-2000; 2000WO-CA00354.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 neoplasm; diagnosis; EST; expressed sequence tag; ds
                                                                                                                                                                                                                                                                                                                                                           disease and other neurodegenerative diseases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12-OCT-2000
                                                                                                                                                                                                                                                                                                                    Example 1; Page 62; 79pp; English.
                                                                                                                                                                                                                                                                                                                                                                             Isolated presenilin associated membrane proteins and nucleic acids encoding them, useful for investigating and diagnosing Alzheimer's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (UTOR ) UNIV TORONTO GOVERNING COUNCIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 attcctaattgccagcaaagagcttgagttcatcacgctgatcgtgggcttc 172
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                                     neurodegenerative and other diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 gagctccacagaatactctacgtgggcggagagcgcgtggaaagacatcccagctcggat 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gagototactgaatactotacatggactgagagocgotggaaagatatocgtgocoggat 2121
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99US-0173826.
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83.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fraser PE;
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Pred. No. 1.6e-25;
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Sequence 425 BP; 137 A; 74 C; 113 G; 101 T; 0 other;

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RESULT
AAA37887
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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                     neurodegenerative disease; Alzheimer's disease; Lewy body variant; parkinson's disease-dementia complex; neuropsychiatric disease; schizophrenia; age-associated memory loss; developmental disorder;
                                                                                                                                                                                                                                                                                                                                                  D. melanogaster PAMP coding sequence
                                                                                                                                                                                                                                                                                                                                                                                                                        AAA37887 standard; DNA; 2942 BP
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WPI; 2000-665001/64
P-PSDB; AAY97551.
                                   St George-Hyslop PH,
                                                                               01-APR-1999;
30-DEC-1999;
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                                                                                                                                                                   WO200060069-A1.
                                                                                                                                                                                                                                                    Drosophila melanogaster
                                                                                                                                                                                                                                                                           neoplasm; diagnosis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          395 CCTTCTGTCCTTCCATCCTGCCCTGTACTGCCCTCTGACTCCACTGTCACCCGACACCC
                                                         (UTOR ) UNIV TORONTO GOVERNING COUNCIL
                                                                                                                                           12-OCT-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tcaaactacattgagcccctgaggacaggggcatctctgggctgagcctactgtctcct
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTATCCCACCTCCAGCCCACAGTGCTCAGTTGTACTTTTTATTATTAAACTATAATTAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCCACTGTCCTTTCTCCAGGTGTGCAGATGGCATGTTAGTGTGGGCACGCTGTTAAGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241;
                                                                                                                                                                                                                                                                                                                          presenilin associated membrane protein; immunogen
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                                                                                 99US-0127452.
99US-0173826.
                                                                                                                                                                                                                   Location/Qualifiers 83..2170
                                                                                                                                                                                           /product= PAMP
                                                                                                                                                                                                         /*tag=
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Best Local
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    730
                       823 tgccacctgcatgcggcgcagctccatc 850
                                                                          670 cgcgctgcgtagcttgtgcgccgtcgaggtcaagtcctttatgtccgccgctgtcaacac 729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Isolated presenilin associated membrane proteins and nucleic acids encoding them, useful for investigating and diagnosing Alzheimer's disease and other neurodegenerative diseases -
                                                                                                                                                                                                                                                                                                                                                                                                                            433 cacgaaccagatgaagcagttctcgcacgaactcaactgccccaatcagtacagcggcct 492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2942 BP; 823 A; 729 C; 594 G; 796 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      neurodegenerative and other diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 9; Page 73-75; 79pp; English.
                                                                                                                                                                                                                                                                                                                                                         493
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                                                                                                                                                                                           tgaaaccaaagtcatcaagcagtgctatcaagatcacaacctgagtcagaatggctcagc 762
                                                                                                                                                                                                                                                                                            999caat99tttggcttatgaagactttagtttccccatctttcttcttgaagatgaaaa
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cgaggtctgtatgcgccgcaccaacttc 757
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Pred. No. 0.00014;
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                                                                                             35755 toto--coattttattaaataataatttaataacataattttatatatgtttatatta
                                                                                                                                             2621 ctctgctcctcaccccacccct 2643
                                                             2501 actcatgccagattttgggattacaaatagaagcttcttgctcctgtttaactccctagt 2560
                                                                                                                                                           also be used to perform subcellular and histochemical localisation studies, and to block the function of PKD1. Ab are also useful in rational drug design studies to identify and test inhibitors of
                                                                                                                                                                                                                                                                                                                                                 The present sequence is the human polycystic kidney disease 1 (PKDI) gene. The PKDI gene or polypeptide may be used to treat autosomal dominant polycystic kidney disease (APKD), and identify carriers of mutant PKDI genes, i.e. subjects susceptible to APKD. Antibodies (Ab) that distinguish between normal and mutant PKDI sequences can also be used in diagnostic tests. Anti-PKDI Ab may
                                                                                                                                                                                                                                                             Sequence 53526 BP; 8486 A; 17665 C; 15768 G; 11607 T; 0 other;
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Qian F;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 2; Pages 90-118; 257pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human polycystic kidney disease gene, PKD1 - useful to treat and diagnose human autosomal or adult onset polycystic kidney disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Qian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1998-018511/02
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24-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; polycystic kidney disease 1; PKD1; treatment; autosomal dominant polycystic kidney disease; APKD; ss
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                                                                                                                                                                                                     Conservative
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Search completed: June 27, Job time: 6466 sec 2001, 16:53:52

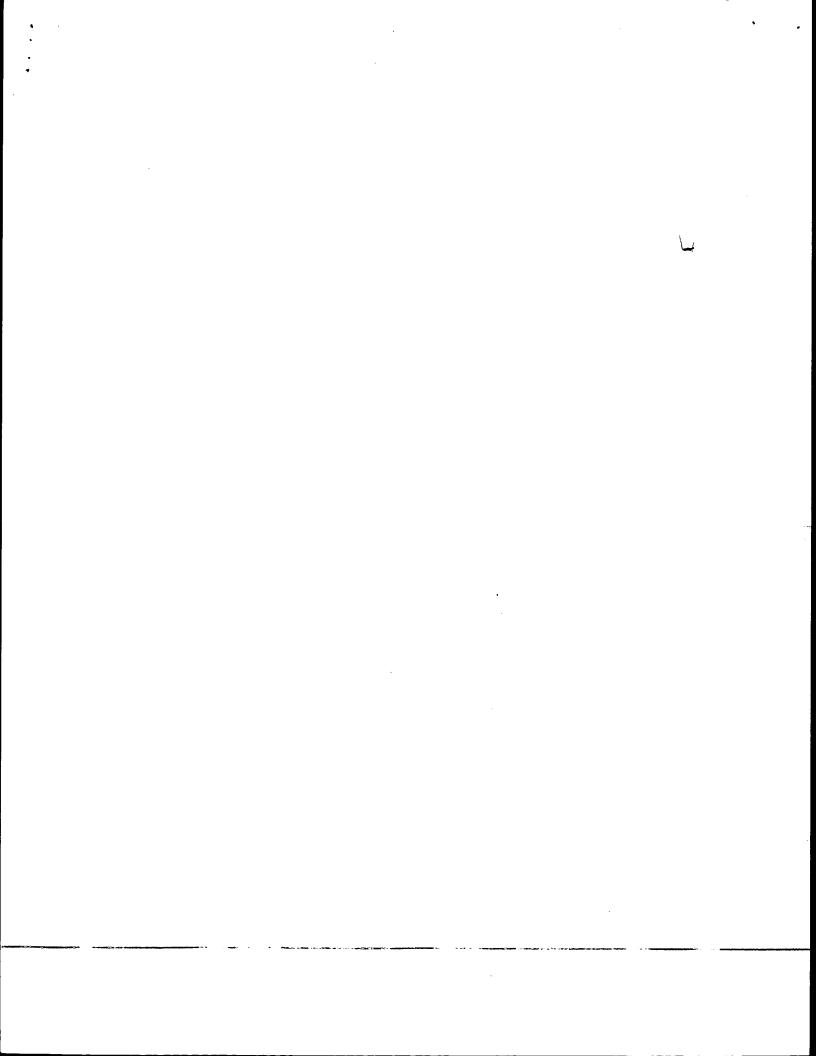
AAT94101 ID AAT9 XX

AAT94101 standard; DNA; 53526 BP.

RESULT

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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

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Sequence:
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Maximum DB seq length: 200000000
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
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US-08-967-727-5
US-08-967-727-5
US-08-967-727-5
US-08-911-020-3
US-08-911-020-3
US-08-918-8268-13
US-09-247-3738-3
US-09-182-816-22
US-09-182-816-24
US-09-182-816-10
US-08-545-1968-10
US-08-545-1968-12
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| RESULT 1 US-08-32-463-14 Sequence 14, Application US/08232463 Patent No. 5670367 GENERAL INFORMATION: APPLICANT: DORNER, F. APPLICANT: DORNER, F. APPLICANT: FALKNER, F. G. APPLICANT: PRODUNCES: SOLEY APPLICANT: RECOMBINANT FOWLPOX VIRUS INTER: 2313-0299 COMPUTER READABLE FORM: AEDIUM TYPE: Ploppy disk COMPUTER READABLE FORM: AEDIUM TYPE: Floppy disk COMPUTER READABLE FORM: AEDIUM TYPE: Ploppy disk COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PATENTIAN RELEASE #1.0, Version #1.25 CURENT APPLICATION NUMBER: US/08/232,463 FILING DATE: APPLICATION NUMBER: US/08/232,463 FILING DATE: 26-AUG-1991 AFTORNEY/AGENT INFORMATION: NAME: BENT, SCEPHEN A. REGISTRATION NUMBER: 29,768 REFERRNCE/DOCKET NUMBER: 39,768 RESISTRATION INFORMATION: TELEFAX: (703)683-4109 INFORMATION FOR SEQ ID NO: 14: SEQUENCE CHARACTERISTICS: LENGTH: 7218 base pairs TYPE: NUCLEIC acid STRANDEDNESS: single TOPOLOGY: linear IMMEDIATE SOURCE: CLONE: pTZ9T-F1s US-08-232-463-14 | C 28 38 1.3 688 6 5498694-3 C 30 38 1.3 1493 1 US-08-340-820-24 C 31 37.6 1.3 1493 1 US-08-628-417-5 C 31 37.6 1.3 294 1 US-08-628-417-6 C 33 37.6 1.3 294 1 US-08-628-417-6 C 34 37.6 1.3 7286 4 US-09-331-581-3 C 34 37.6 1.3 7286 4 US-09-331-581-3 C 37 37.4 1.3 745 2 US-08-332-766A-16 C 37 37.4 1.3 2294 1 US-08-332-766A-16 C 39 37.4 1.3 2290 1 US-08-378-313-24 C 39 37.4 1.3 3238 5 PCT-US94-10080-5 C 40 37.4 1.3 5173 1 US-08-242-677-1 C 40 37.4 1.3 5852 1 US-08-6738-2 C 43 37.2 1.3 966 2 US-08-821-994-63 C 43 36.8 1.2 1441 4 US-08-821-994-63 C 44 36.8 1.2 1712 US-08-731-272A-29 |
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| | Patent No. 5498694 Sequence 24, Appl Sequence 24, Appl Sequence 5, Appl: Sequence 6, Appl: Sequence 14, Appl: Sequence 16, Appl: Sequence 16, Appl: Sequence 17, Appl: Sequence 17, Appl: Sequence 17, Appl: Sequence 17, Appl: Sequence 27, Appl: Sequence 28, Appl: Sequence 64, Appl: Sequence 63, Appl: Sequence 69, Appl: |

; STRANDEDNESS: single ; TOPOLOGY: linear ; MOLECULE TYPE: DNA (genomic) US-08-658-136-2

TYPE:

nucleic acid

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US-08-658-136-2
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                                   TELEFAX: 508-872-5415
INFORMATION FOR SEQ ID NO: 2:
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                                                                REFERENCE/DOCKET NUMBER: GETELECOMMUNICATION INFORMATION: TELEPHONE: 508-872-8400
                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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ADDRESSEE: GENZYME CORPORATION
                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: POLYCYSTIC KIDNEY DISEASE GENE NUMBER OF SEQUENCES: 58
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TITLE OF INVENTION: PO
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                                                                                                                  NAME: LASSEN, ELIZABETH REGISTRATION NUMBER: 31
                                                                                                                                                                      CLASSIFICATION: 435
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                                                                                                                                                                                                        APPLICATION NUMBER:
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LANDES, GREGORY M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 114;
                                                                                                                TELEFAX: 508-872-5415 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    35873 CTCTTCCTTTTCCTCTCCCCT 35895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              35755 TCTC--CCCTTTTCTTCCCTCCTTCCTTCCCCCCTCCTTTTCTCTGTTTCTCTTCC 35812
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                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 53577 base pairs
                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: KLINGER, KATHERINE W
APPLICANT: LANDES, GREGORY M
APPLICANT: BURN, TIMOTHY C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2501 actcatgccagattttgggattacaaatagaagcttcttgctcctgtttaactccctagt 2560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
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                             STRANDEDNESS:
TOPOLOGY: lin
                                                                                                                                                                                 NAME: LASSEN, ELIZABETH REGISTRATION NUMBER: 31. REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                 FILING DATE: CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: ONE MOUNT CITY: FRAMINGHAM STATE: MASSACHUS
                                                                                                                                                TELEPHONE:
                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/658,136
                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: 1
ZIP: 0170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
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                                                               nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                    MASSACHUSETTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               ONE MOUNTAIN ROAD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BURN, TIMOTHY C
CONNORS, TIMOTHY D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                 linear
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                                                                                                                                                508-872-8400
              DNA (genomic)
                                             single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POLYCYSTIC KIDNEY DISEASE GENE
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Pred. No. 0.0025;
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Best Local Similarity
Matches 114; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION: APPLICANT: Boon,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   35868 CTCTTCCTTTTCCTCTCCCCT 3589
                                                                           TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2501 actcatgccagattttgggattacaaatagaagcttcttgctcctgtttaactccctagt 2560
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                                                                                                                                                                                                    APPLICATION NUMBER: 07/7
FILING DATE: 23-May-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 07/764,364
FILING DATE: 23-SEPTEMBER-1991
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Wordperfect CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                             TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 688-9200
                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
TOPOLOGY: 11
                                                                                                                                                                                                                                                            FILING DATE: 9-JULY-1991 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITATE: No. 10022
                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 07/728,838 FILING DATE: 9-JULY-1991
                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/07/807,043B FILING DATE: 19911212
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                              STRANDEDNESS:
                                                                                                                                                                           NAME: Hanson, No. 5342774man D. REGISTRATION NUMBER: 30,946
                                                                                                                                                               REFERENCE/DOCKET NUMBER:
                                                               LENGTH:
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                                                NUCLEIC ACID
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805 Third Avenue
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VENTION: Tumor Rejection Antigen Precursors, Tumor
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                                                               4698 base pairs
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                  linear
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genomic DNA
                             singular
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                                                                                                                                                               LUD 253.3
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 5, Application US/08299849B
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Isolated Nucleic Acid Molecules Useful in TITLE OF INVENTION: Determining Expression Of A Tumor Antigen Precursor
                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/728,838
APPLICATION NUMBER: 9-JULY-1991
                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 26-MARCH-1993
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 23-SEPT
                                    TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 688-9200
                                                                                                                             APPLICATION NUMBER: 07/7
FILING DATE: 23-May-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                          PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/299 FILING DATE: 1-SEPTEMBER-1994 CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 08/037,230
                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: FILING DATE: 12-DEC
                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: PCT/I
FILING DATE: 22-MAY-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Wordperfect
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                    TELEPHONE:
                                                                           REFERENCE/DOCKET NUMBER:
                                                                                       NAME: Hanson, No. 5612201man D. REGISTRATION NUMBER: 30,946
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New York City
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                    (212)
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                    838-3884
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                                                                                                                                                                          07/705,702
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                                                                           LUD 5355
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SEQUENCE CHARACTERISTICS: LENGTH: 4698 base pairs

STRANDEDNESS: TYPE:

linear

0,

single

nucleic acid

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Patent No. 5925729
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                    ATTORNEY/AGENT INFORMATION
                                                                                                                          PRIOR APPLICATION DATA:
                                                                       PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Boon-Falleur, Thierry; Van der Bruggen, Thierry; APPLICANT: Van den Eynde, Beno t; Van Pel, Aline; De Plaen, Etienne; APPLICANT: Lurquin, Christophe; Chomez, Patrick; Traversari, Catia TITLE OF INVENTION: Tumor Rejection Antigen Precursors, Tumor TITLE OF INVENTION: Rejection Antigens and Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
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CORRESPONDENCE ADDRESS:
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MOLECULE TYPE:
                                                                                      APPLICATION NUMBER: 07/728,838 APPLICATION NUMBER: 9-JULY-1991
                                                    APPLICATION NUMBER:
                                                                                                                                            APPLICATION NUMBER: 07/764,364 FILING DATE: 23-SEPTEMBER-1991
                                                                                                                                                                                                   FILING DATE: 12-DECEMBER-1991
                                                                                                                                                                                                                                                        APPLICATION NUMBER: PCT/
FILING DATE: 22-MAY-1992
                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/142/368A FILING DATE: 02-MAY-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE:
                                                                                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE:
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Hanson, No. 5925729man D
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805 Third Avenue
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                                                  07/705,702
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Pred. No. 0.011;
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Best Local Similarity
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Gaugler, B atrice; Van den Eynde, Beno t;
APPLICANT: van der Bruggen, Pierre; Boon-Falleur, Thierry
TITLE OF INVENTION: Isolated Nucleic Acid Molecules Coding
TITLE OF INVENTION: Tumor Rejection Antigen Precure
                              PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                             APPLICATION NUMBER:
FILING DATE: 22-MAY-
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                        SOFTWARE: Wordperfect CURRENT APPLICATION DATA:
                                                                                                                                                                                    PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                  STATE: New 10022
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REFERENCE/DOCKET NUMBER: LU
TELECOMMUNICATION INFORMATION:
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                                                                                                                    (IOR APPLIANCE TO NUMBER: 08/03/,200 APPLICATION NUMBER: 08/03/,200 FILING DATE: 26-MARCH-1993
FILING DATE: 26-MARCH-1993
FILING DATE: PCT/US92/04354
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                                                              APPLICATION NUMBER: 07/807,04 FILING DATE: 12-DECEMBER-1991
                 FILING DATE:
                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
                                                                                                                                                                                                                         FILING DATE
                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: PC-DOS
                                                                                                                                                                                                                                                                                                               COMPUTER:
                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/967,727
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                                                                                                                                                                                                                                                                                                                         Diskette,
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          23-SEPTEMBER-1991
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                                                                                 07/807,043
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SEQUENCE CHARACTERISTICS:
LENGTH: 4698 harr
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Best Local Similarity 50.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 5, Application US/08037230D Patent No. 6235525
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APPLICANT: Gaugler, B atrice
APPLICANT: van der Bruggen,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: LUTELECOMMUNICATION INFORMATION: (212) 688-9200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 23-MAY-1991
ATTORNEY/AGENT INFORMATION:
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FILING DATE: 9-JULY-1991
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2739 CTTTCCCCTTCCCCTATGCCCTCTACTCTACTTGA 2773
                                                                                                                                                OPERATING SYSTEM: PC-DOS
SOFTWARE: WORDPERFECT
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Isolat
                                                                      PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                    STATE: No. 10022
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                                                                                        FILING DATE: 26 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                        STREET:
                                                                                                        APPLICATION NUMBER: US/08/037,230D
FILING DATE: 26-MARCH-1993
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                      New York City
                                                                                                                                                                                                                                                                                                                      E: Felfe & Lynch
805 Third Avenue
                                                                                                                                                                                                                                                                                                                                                                                              Gaugler, B atrice; Van den Eynde, Beno t;
van der Bruggen, Pierre; Boon-Falleur, Thierry
VENTION: Isolated Nucleic Acid Molecules Coding For
VENTION: Tumor Rejection Antigen Precursor Mage-3 And Uses Thereof
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07/807,043
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                                                                                                                                                                                                                                360 kb storage
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/705,702
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APPLICANT:
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LENGTH: 4698 base pairs
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ATTORNEY/AGENT INFORMATION:
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ZIP: 22040-0/-.
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
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                                                                                                                                                                                    TITLE OF INVENTION: method TITLE OF INVENTION: pulps NUMBER OF SEQUENCES: 7
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                                                                                                                                                                                                                      TITLE OF INVENTION: Mannanase enzymes, genes coding for them, TITLE OF INVENTION: methods for isolating the genes, and meth
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                                                                                                                                                                    CORRESPONDENCE ADDRESS:
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                                                                                                                                   STREET:
                                                                                 COUNTRY:
                                                                                                                                                   ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nucleic acid
                                                                                                   Falls Church : VA
                                                                                                                                 E: Birch, Stewart, Kolasch and Birch
                                                                                                                                                                                                                                                                                                         Siika-aho, Mat
Viikari, Liisa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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Marjatta, Ranua
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                                                                                                                                                                                                                             and methods
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RESULT 10
US-08-911-020-3/c
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US-08-341-568-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                          SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS: Birch, St
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                  PRIOR APPLICATION DATA;
                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION:
TITLE OF INVENTION:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
TELEPAX: 7070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Murphy Jr, Gerald M
REGISTRATION NUMBER: 28,97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                           APPLICATION NUMBER: FILING DATE: 13-AUC CLASSIFICATION: 435
 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 223 TTGATATATATATATTCATCAAAAACGCCCCCCCCCC 185
                                                                                                                                                                                                                         CITY: Falls Church
                                                                                                                                                                               ZIP: 22040-0747
                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                              STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (703) 205-800
TELEFAX: (703) 205-8050
TELEX: 248345
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STRANDEDNESS: sing
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SOFTWARE: PatentI
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Viikari, Liisa
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Saloheimo, Anu
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                                               13-AUG-1997
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                                                                                                                                                                                                                                                                                                                     Mannanase enzymes, genes coding for them, methods for isolating the genes, and methods for bleaching
                                                                                                                                                                                                                                                                                                       methods for isolating lignocellulosic pulps
                                                                                                                                                                                                                                                        Stewart, Kolasch and Birch
                                                                                            Release #1.0, Version #1.30
US 08/341,568
                                                              US/08/911,020
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Chang, Andy C M
APPLICANT: Williams, Keith L
TITLE OF INVENTION: Improved Plasmid Vectors for Cellular
TITLE OF INVENTION: Slime Moulds of the Genus Dictyostelliv
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
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              TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Feeney, Joanne Longo
REGISTRATION NUMBER: 35,13
                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                            PRIOR APPLICATION DATA;
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ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 289 base pairs
TYPE: nucleic acid
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REFERENCE/DOCKET NUMBER: 365-262P
TELECOMMUNICATION INFORMATION:
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ATTORNEY/AGENT INFORMATION:
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                                                                  REGISTRATION NUMBER: 35,134
REFERENCE/DOCKET NUMBER: RIC
                                                                                                                                     APPLICATION NUMBER: AU pJ 7187
APPLICATION NUMBER: PCT/AU90/00530
FILING DATE: 02-NOV-1989
                                                                                                                                                                                                             APPLICATION NUMBER: U: FILING DATE: 19920625
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                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                          STREET: One Liberty CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                               STATE:
                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 63.6%;
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STRAIN: QM9414
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REGISTRATION NUMBER: 28,97
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Chang, Andy C M
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             RESULT 13
US-08-487-826B-13/c
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                                                                                                                                                                                                                                                                                   ; NAME/KEY: misc_feature
; LOCATION: (1)..(2409)
; OTHER INFORMATION: N is A, T, G or C.
US-09-293-322C-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Pallas, David C
APPLICANT: Du, Xianxing
TITLE OF INVENTION: Coding Sequence for Protein Phosphatase Methylesterase,
Patent No. 6232110
TITLE OF INVENTION: Recombinant DNA Molecules and Methods
FILE REFERENCE: 105-97
CURRENT APPLICATION NUMBER: US/09/293,322C
CURRENT FILING DATE: 1999-04-16
PRIOR APPLICATION NUMBER: US 60/082,202
PRIOR FILING DATE: 1998-04-17
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 8
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                                                                                                                                                                                                                       Query Match 1.4%;
Best Local Similarity 64.2%;
Sequence 13, Application US/08487826B
                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 17
                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Mus musculus
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LENGTH: 5852 base pairs
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                                                                                                            2910 atatatataattaggtttcattaaaatagattat 2944
                                                                                                                                            2346 GTTGGGAGATATTTATTTTCTTTAAACAAGATCAT 2312
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US-09-247-373B-33/c

; Sequence 33, Application US/09247373B

; Patent No. 6168954.
             GENERAL INFORMATION:
APPLICANT: MCGONIGLE, BRIAN
APPLICANT: O'KEEFE, DANIEL
TITLE OF INVENTION: SCYBEAN GLUTATHIONE-S-TRANSFERASE ENZYMES
FILE REFERENCE: CL-1108-A
CURRENT APPLICATION NUMBER: US/09/247,373B
CURRENT APPLICATION NUMBER: 1999-02-10
PRIOR APPLICATION NUMBER: 08/924,747
PRIOR FILING DATE: 1997-09-05
                                                                                                                                                                                                                                                                                                                                                                   US-08-487-826B-13
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                           18325 ATATGTAGAATTACTTTATGTTTTTTTTTTGATAAAAGAAT 18285
NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Peterson, APPLICANT: Su, Xin-z APPLICANT: Wellems,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
APPLICANT:
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: NI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION: NAME: Israelsen, Ned
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOCTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
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LENGTH: 19124 base pai
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STATE: California
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Local Similarity 62.4%;
hes 63; Conservative (
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CLASSIFICATION:
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Miller, Louis H.
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Pred. No. 0.7;
0; Mismatches 38;
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; LOCATION: (159)..(1553)
US-09-182-816-22
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CATION: (1104)
COTHER INFORMATION: M=A OR C
NAME/KEY: unsure
LOCATION: (1116)
COTHER INFORMATION: N=G or A or T or C
US-09-247-373B-33
                                                                                                                                                                                                                                                                                                                                                        EARLIER APPLICATION NUMBER: 08/989,510
EARLIER FILING DATE: 1997-12-12
NUMBER OF SEQ ID NOS: 31
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 22
LENGTH: 1736
TYPE: DNA
                                                                                                                                                       Ouery Match 1.3%; Score 39.6; DB 4; Length 1736; Best Local Similarity 61.8%; Pred. No. 0.27; Matches 63; Conservative 0; Mismatches 39; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 22, Application US/09182816
Patent No. 6143542
GENERAL INFORMATION:
APPLICANT: Wisnewski, Nancy
APPLICANT: Silver, Gary M.
APPLICANT: Lo, Katherine C.
APPLICANT: Brandt, Kevin S.
TITLE OF INVENTION: NOVEL FLEA EPOXIDE HYDROLASE NUCLEIC ACID MOLECULES,
FILE REFERENCE: FC-3-C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Microsoft
SEQ ID NO 33
LENGTH: 1117
TYPE: DNA
ORGANISM: SOYBEAN
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 1.3%; Score 39.8; DB 4; Length 1117; Best Local Similarity 62.6%; Pred. No. 0.19; Mismatches 62; Conservative 0; Mismatches 37; Indels 0,
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CURRENT FILING DATE: 1998-10-29
                                                                                                                                                                                                                                                                                                                           ORGANISM: Ctenocephalides felis FEATURE:
                                                                        1667 TTTTTTTTTTATATTTGACAAGTTTGAAATAAAATCCATATC 1626
                                     2904 ttgtaaatatatatataatgagtttcattaaaatagattatc 2945
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LOCATION: (1101)
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Ota, T., Sugiyama, T., Ishii, S., Suzuki, Y., Saito, K., Yamamoto, J., Nishikawa, T., Nakamura, Y., Nagai, T., Sugano, S., Masuho, Y. and
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Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing: He:
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo,
Helix Research Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba
Tel: 81-438-52-9951
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D.
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Clone distribution: MGC clone distribution information can
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/clone_lib="NIH_MGC_18"
/clone_lib="NIH_MGC_18"
/tissue_type="large cell carcinoma"
/lab_host="0H10B (phage resistant)"
/note="0rgan: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5 adaptor:
GGCACGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
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                                                                      gtttccccatctttcttcttgaagatgalaatgaaaccaaagtcatcaagcagtgctatc 731
                                                                                                               CTCACTGCAGAGAATACAGTGGAATTCGCTGGGCAATGGTTTGGCTTATGAAGACTTTA
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1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3951
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HRI human cDNA project; 5'.& 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fax:
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Genomics Laboratory
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/note="Vector: pwE18SFL3; mRNA from NT2 neuronal |
/note="Vector: pwE18SFL3; mRNA from NT2 neuronal |
cells after 2-weeks retinoic acid (RA) induction"
a 207 c 202 g 206 t 2 others
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/cell_line="NT2"
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/db_xref="taxon:9606"
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                                                                 GGGTTCGGCATCCTCATCTTCTCCCTCATCGTCACCTACTGCATCAATGCCANAGCTGAT 725
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                                                                                                                                  769;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
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National Cancer Institute, Cancer Genome Ana
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="Soares_NFL_T_GBC_S1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon
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/db_xref="taxon:9606"
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CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
                                                                               Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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Tissue Procurement: David N. Louis, M.D.
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National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CLONETECH Laboratories, Inc.
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National Institutes of Health, Mammalian Gene Collection
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Plate: LLCM1564 row: k column: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDNA Library Preparation: CLONETECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (bases 1 to 696)
                                                                                                                                                                                                                                                                                                                                                                             quality sequence stop: 696.
Location/Qualifiers
/db_xref="taxon: your 
                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Homo sapiens
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                                                                                                    910 bp
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                                                                                                               GATTTTGGGATTACAAATAGAAGCTTCTTGCTCCTGTTTAACTCCCTAGTTACCCCACCCT
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Tissue Procurement: David N. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
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/clone_lib="NOI_CGAP_Brn64"
/clone_lib="NOI_CGAP_Brn64"
/tissue_type="glioblastoma with EGFR amplification
/lab_host="DH10B (Tl phage-resistant)"
/note="organ: brain; Vector: pCMV-SPORT6; Site_1;
Site_2: Sall; Cloned unidirectionally. Primer: Oli
Site_2: Sall; Cloned unidirectionally. Primer: Oli
Average insert size 1.57 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP_Library."
a 271 c 179 g 249 t I others
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1 (bases 1 to 807)
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                                                                                                                                                                                                                                                               /tissue_type="choriocarcinoma"
/lab_host="NH10B (phage resistant)"
/note="Organ: placenta; vector: pOTB7; Site_1: XhoI;
/note="Organ: placenta; vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the placetionally cloned into EcoRI/XhoI sites using the following 5 adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
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                                                                               Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NH
Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium
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602288192T1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:4373β31
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Clone distribution: MGC clone distribution information
found through the I.M.A.G.E. Consortium/LLNL at:
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/clone="IMAGE:4373831"
/clone_11b="NIH_MGC_97"
/lab_host="DH10B"
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                                                                                                 ogtgcccggatatttctcatcgccagcaaagagcttgagttgatcaccctgacagtggg
                                                                              CGTGCCCGGATATTTCTCATCGCCAGCAAAGAGCTTGAGTTGATCACCCTGACAGTGGGC
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High quality sequence stop: 656.
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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Tissue Procurement: ATCC
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BF793556
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information
found through the I.M.A.G.E. Consortium/LLNL at:
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/lab_host="pHIOB (phage resistant)"
/note="organ: adrenal gland, Vector: pCMV-SPORT6; Site_1:
NotI; Site_2: Sall; Cloned unidirectionally; oligo-dr
primed. Average insert size 1.229 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
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/clone="IMAGE:4347355"
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Tissue Procurement: Linehan
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National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                        quality sequence start: 27 quality sequence stop: 692.
/organism="Homo sapiens"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/dlone="ImAGE:4310584"
/clone=1b="NIH_M6C_45"
/clone_1b="NIH_M6C_45"
/tissue_type="renal carcinoma (ascites)"
/lab_host="PH10B (phage=resistant)"
/note="Organ: kidney; Vector: poTB7; Site_1: xhoI; Site_2: /note="Organ: kidney; Vector: poTB7; Site_1: xhoI; Site_2: foors; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor:
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602071875F1 NCI_CGAP_Brn67 Homo sapiens
5', mRNA sequence
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Homo sapiens
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                                        BF530600.1 GI:11617963
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97.2%;
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                     2193 tcatcgtcacctactgcatcaatgccaaagctgatgtccttttcattgctccccggggagc 2252
                                                                                                                                                                                          2073 aatactctacatggactgagagccgctggaaagatatccgtgcccggatatttctcatcg 2132
                                                                                                                                                                                                                                                                           2013 ctgcacgattagccagggccttgtctcctgcctttgaactgagtcagtggagctctactg 2072
                                                                                                                                                                                                                                                                                                                                                          1893 agcagtgccaggatccaagtaaagtcccaagtgaaaacaaggatctgtatgagtactcat 1952
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476 TCATCGTCACCTACTGCATCAATGCCAAAGCTGATGTCCTTTTCATTGCTCCCCGGGAGC 535
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                                                                              CCAGCAAAGAGCTTGAGTTGATCACCCTGACAGTGGGCTTCGGCATCCTCATCTTCTCCC 475
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                                                                                                                                                                    AATACTCTACATGGACTGAGAGCCGCTGGAAAGATATCCGTGCCCGGATATTTCTCATCG
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Tissue Procurement: David N. Louis, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LENL)
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Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
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/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT
Average insert size 2.3 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
a 274 c 212 g 226 t
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/clone="IMAGE:4214778"
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93.8%;
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Pred. No. 4.3e-158;
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2276 ggaccscagcttttcttgccagctcagcagttcacttcctagagcatctgtcccactgg
                                                                  2216 gccaaagctgatgtccttttcattgctccccgggagccaggagctgtgtcatactgagsa 2275
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Plate: LLCM1185 row: m column: 17
High quality sequence stop: 742.
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Tissue Procurement: Linehan
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 813)

NIH-MGC http://mgc.nci.nih.gov/.

Mational Institutes of Health, Mammalian Gene Collection (MGC)
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1999)
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602185971F1 NIH_MGC_45
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                                                                                                                                      Conservative
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/lab_host="DH10B (phage=resistant)"
/note="regan: kidney; vector: pOTB7; Site_1: xhof; Site_2:
ECORI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GCACGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library. |"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="IMAGE:4310584"
/clone_lib="NIH_MGC_45"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:9606"
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                                                                                                                                                      21.1%; 97.5%;
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                                                                                                                                                 Score 623; DB 150; Length 813; Pred. No. 5e-157;
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Tissue Procurement: DCTD/DTP/Gazdar
CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
                                                                                                                                                                                                                        BE788789 820 bp mRNA
601475883F1 NIH_MGC_68 Homo
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National Institutes of Health, Mammalian
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                                                                                   Contact: Robert Strausberg, Ph.D.
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/lab_host="DH108 (phage-resistant)"
/note="Organ: lung; Vector: pCMV-SPORT6; Site_1: NC Site_2: Sall; Cloned unidirectionally. Primer: Oli Average insert size 1.8 kb. Library constructed to Technologies."

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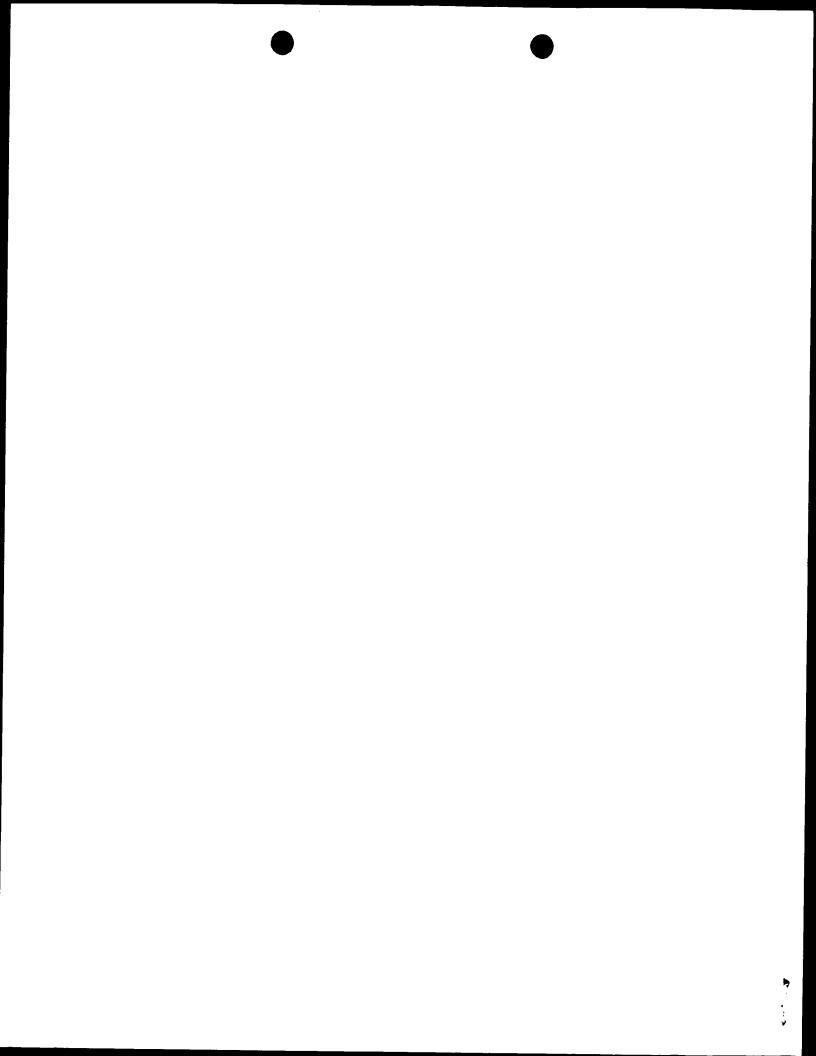
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Prediction of the coding sequences of unidentified human genes.VI.
The coding sequences of 80 new genes (KIAA0201-KIAA0280) deduced is analysis of cDNA clones from human cell line KG-1 and brain unpublished (1996)
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                               Homo sapiens male bone marrow myeloblast cell_line:KG-1 cDNA mRNA, clone_lib:pBluescript II SK clone:HA7036.
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Human mRNA for KIAA0253 gene, partial cds.
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AATRIDSRSFFWNVAPGAESAVASTYOLAARALOKARDYTLERWHFUFFORFY
DYIGSSRWYVDMEKGKFPVOLENVDSFVELQOYLRTSLELMHTDPVSGKRESYRNO
VEDLLATLEKSGAGVPAVILRRPNGSPDLFDSSLORFLRARNISGVYLANDSGAFBNK
YYOSIYDTAERIKINSPFBULAVPTOTAKALADVATVLGRALVELAGGTNFSD
TVQADPQTVTRLLYGFLIKANNSWFOSILRQDLRSYLGDGPLQHYIAVSSPTNTTYVV
QYALANLTGTVVNLTREGCODPSKVPSENKDINEYSTSWYGGPLHSNETDRLPRCVRSTA
RLARALSPAFELSGWSSTEYSTWTESRWKDIRARIFLIASKELELITLTVGFGILIFS
LIVTYCINAKADVTRARGGANSY*

765 C 646 9 746 t
IOWNSLGNGLAYEDFSFPIFLLEDENETKVIKQCYQDHNLSQNGSAPTFPLCAMQLFS
HMHAVISTATCMRRSSIQSTFSINPEIVCDPLSDYNVWSMLKPINTGTLKPDDRVVV
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Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Uso
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